

Refine Search

Search Results -

Term	Documents
HEAT	3294346
HEATS	122347
SHOCK	419667
SHOCKS	72211
PROTEINS	246473
PROTEIN	383106
(35 AND ((HEAT ADJ SHOCK) ADJ PROTEINS)).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	29
(L35 AND HEAT SHOCK PROTEINS).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	29

Database:

US Pre-Grant Publication Full-Text Database
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Search:

L36

Refine Search

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DATE: Wednesday, April 06, 2005 [Printable Copy](#) [Create Case](#)

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DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ

L36 L35 and heat shock proteins

29 L36

L35 L34 and @py<2003

256 L35

L34 2-D gel

627 L34

<u>L33</u>	US 6331388 B1	2	<u>L33</u>
<u>L32</u>	L31 and protein same degradation same prevention	35	<u>L32</u>
<u>L31</u>	heat shock proteins and protease	2727	<u>L31</u>
<u>L30</u>	heat shock protein same prevent same protein same degradation	6	<u>L30</u>
<u>L29</u>	heat skock proteins same (2-D gel electrophoresis) same prevent same degradation same protein	0	<u>L29</u>
<u>L28</u>	L27 and prevent protein degrdation	0	<u>L28</u>
<u>L27</u>	L26 and protease	493	<u>L27</u>
<u>L26</u>	L25 and composition	764	<u>L26</u>
<u>L25</u>	L24 and @py<2003	847	<u>L25</u>
<u>L24</u>	L23 and method	2184	<u>L24</u>
<u>L23</u>	L22 and prevent	2184	<u>L23</u>
<u>L22</u>	heat shock proteins and degradation	2742	<u>L22</u>
<u>L21</u>	2-D gel same heat shock proteins	8	<u>L21</u>
<u>L20</u>	2-D gel same heat shock proteins same use same degradation	0	<u>L20</u>
<u>L19</u>	L15 and protein degradation	5	<u>L19</u>
<u>L18</u>	L15 and HSP26	0	<u>L18</u>
<u>L17</u>	L15 and IbpB	0	<u>L17</u>
<u>L16</u>	L15 and IbpA	0	<u>L16</u>
<u>L15</u>	L14 and electrophoresis	64	<u>L15</u>
<u>L14</u>	L13 and L11	68	<u>L14</u>
<u>L13</u>	heat shock proteins	6432	<u>L13</u>
<u>L12</u>	L11 and heat shock proteins HSP	5831	<u>L12</u>
<u>L11</u>	2-D gel	627	<u>L11</u>
<u>L10</u>	2-D gel same heat shock proteins	8	<u>L10</u>
<u>L9</u>	US 5320951	3	<u>L9</u>
<u>L8</u>	US 5175096	2	<u>L8</u>

DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ

<u>L7</u>	decorin same clot formation same kit	2	<u>L7</u>
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DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ

<u>L6</u>	decorin same clot formation	4	<u>L6</u>
<u>L5</u>	decorin same antithrombotic	3	<u>L5</u>
<u>L4</u>	decorin same anticoagulating	3	<u>L4</u>
<u>L3</u>	L2 and N-terminal	36	<u>L3</u>
<u>L2</u>	decorin same glycosaminoglycan	96	<u>L2</u>
<u>L1</u>	antithrombotic same decorin same proteoglycan same glycosaminoglycan	0	<u>L1</u>

END OF SEARCH HISTORY

Refine Search

Search Results -

Term	Documents
HSP	3955
HSPS	2141
(16 AND HSP).PGPB,USPT.	3
(L16 AND HSP).PGPB,USPT.	3

Database:

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Search:

L17

Search History

 DATE: Wednesday, April 13, 2005 [Printable Copy](#) [Create Case](#)

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<i>DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<u>L17</u>	L16 and HSP	3	<u>L17</u>
<u>L16</u>	L15 and @py<2003	59	<u>L16</u>
<u>L15</u>	proteomes same gel electrophoresis	400	<u>L15</u>
<u>L14</u>	L13 and heat shock proteins	3	<u>L14</u>
<u>L13</u>	L12 and @py<2003	37	<u>L13</u>
<u>L12</u>	L11 and 2-D gel	162	<u>L12</u>
<u>L11</u>	proteomes	1371	<u>L11</u>
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<u>L10</u>	L9 and @py<2003	72	<u>L10</u>
<u>L9</u>	L7 and gel electrophoresis	118	<u>L9</u>
<u>L8</u>	L7 and protein degradation	9	<u>L8</u>

<u>L7</u>	small heat shock proteins	201	<u>L7</u>
<u>L6</u>	L5 and @py<2003	16	<u>L6</u>
<u>L5</u>	L4 and degradation	57	<u>L5</u>
<u>L4</u>	L3 and composition	158	<u>L4</u>
<u>L3</u>	L2 and py<2003	201	<u>L3</u>
<u>L2</u>	small heat shock proteins	201	<u>L2</u>
<u>L1</u>	small heat shock proteins composition	0	<u>L1</u>

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(ROSPATENT) added to list of core patent offices covered
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data from INPADOC
NEWS 5 FEB 28 BABS - Current-awareness alerts (SDIs) available
NEWS 6 FEB 28 MEDLINE/LMEDLINE reloaded
NEWS 7 MAR 02 GBFULL: New full-text patent database on STN
NEWS 8 MAR 03 REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS 9 MAR 03 MEDLINE file segment of TOXCENTER reloaded
NEWS 10 MAR 22 KOREAPAT now updated monthly; patent information enhanced
NEWS 11 MAR 22 Original IDE display format returns to REGISTRY/ZREGISTRY
NEWS 12 MAR 22 PATDPASPC - New patent database available
NEWS 13 MAR 22 REGISTRY/ZREGISTRY enhanced with experimental property tags
NEWS 14 APR 04 EPFULL enhanced with additional patent information and new
fields
NEWS 15 APR 04 EMBASE - Database reloaded and enhanced

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MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

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FILE COVERS 1907 - 6 Apr 2005 VOL 142 ISS 15
FILE LAST UPDATED: 5 Apr 2005 (20050405/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=> s @-D gel
    2189555 D
    458143 GEL
    92335 GELS
    494175 GEL
        (GEL OR GELS)
L1      1052 @-D GEL
        (D(W)GEL)

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    1211478 HEAT
    53338 HEATS
    1225064 HEAT
        (HEAT OR HEATS)
    2 SKOCK
    1200566 PROTEINS
    4 PROTEINSES
    1200570 PROTEINS
        (PROTEINS OR PROTEINSES)
L2      0 HEAT SKOCK PROTEINS
        (HEAT(W)SKOCK(W)PROTEINS)

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    53338 HEATS
    1225064 HEAT
        (HEAT OR HEATS)
    2 SKOCK
    1729771 PROTEIN
    1200566 PROTEINS
    2008504 PROTEIN
        (PROTEIN OR PROTEINS)
L3      0 HEAT SKOCK PROTEIN
        (HEAT(W)SKOCK(W)PROTEIN)

=> s chapaerone
    0 CHAPAERONE
L4      0 CHAPAERONE

=> s HSP
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    2046 HSPS
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L5 15629 HSP
 (HSP OR HSPS)

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(FILE 'HOME' ENTERED AT 13:31:18 ON 06 APR 2005)

FILE 'CAPLUS' ENTERED AT 13:31:28 ON 06 APR 2005

L1 1052 S @-D GEL
L2 0 S HEAT SKOCK PROTEINS
L3 0 S HEAT SKOCK PROTEIN
L4 0 S CHAPAERONE
L5 15629 S HSP

=> s L1 and L5

L6 42 L1 AND L5

=> s L6 and protein

1729771 PROTEIN
1200566 PROTEINS
2008504 PROTEIN
 (PROTEIN OR PROTEINS)

L7 42 L6 AND PROTEIN

=> s L7 and prevention and denaturation

278897 PREVENTION
122 PREVENTIONS
278952 PREVENTION
 (PREVENTION OR PREVENTIONS)
34803 DENATURATION
158 DENATURATIONS
34846 DENATURATION
 (DENATURATION OR DENATURATIONS)

L8 0 L7 AND PREVENTION AND DENATURATION

=> s L7 and prevention

278897 PREVENTION
122 PREVENTIONS
278952 PREVENTION
 (PREVENTION OR PREVENTIONS)

L9 0 L7 AND PREVENTION

=> d his

(FILE 'HOME' ENTERED AT 13:31:18 ON 06 APR 2005)

FILE 'CAPLUS' ENTERED AT 13:31:28 ON 06 APR 2005

L1 1052 S @-D GEL
L2 0 S HEAT SKOCK PROTEINS
L3 0 S HEAT SKOCK PROTEIN
L4 0 S CHAPAERONE
L5 15629 S HSP
L6 42 S L1 AND L5
L7 42 S L6 AND PROTEIN
L8 0 S L7 AND PREVENTION AND DENATURATION
L9 0 S L7 AND PREVENTION

=> d L7 1-10 ibib,abs

L7 ANSWER 1 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2005:133528 CAPLUS

DOCUMENT NUMBER: 142:238591

TITLE: Proteomic profiling of human stem cells derived from
 umbilical cord blood

AUTHOR(S) : Zenzmaier, Christoph; Gesslbauer, Bernd; Grobuschek, Nina; Jandrositz, Anita; Preisegger, Karl-Heinz; Kungl, Andreas J.
CORPORATE SOURCE: Lifecord Inc., Graz, A-8010, Austria
SOURCE: Biochemical and Biophysical Research Communications (2005), 328(4), 968-972
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB CD34+ prepns. from five different umbilical cord samples were compared with respect to their proteome profile using 2-D gel electrophoresis. Fifty-two **protein** spots were found to match in all prepns. referring to the high heterogeneity of such samples indicating a not fully developed (or instable) proteome of stem cells. All matching spots were subjected to in-gel digestion and nano-LC-MS/MS sequence anal., from which 22 **proteins** were unambiguously identified.
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:1067027 CAPLUS
TITLE: Differential signatures of **protein** expression in marmoset liver and thymus induced by single-dose TCDD treatment
AUTHOR(S) : Oberemm, Axel; Meckert, Christine; Brandenburger, Linda; Herzig, Andrea; Lindner, Yvonne; Kalenberg, Kareen; Krause, Eberhard; Ittrich, Carina; Kopp-Schneider, Annette; Stahlmann, Ralf; Richter-Reichhelm, Hans-Bernhard; Gundert-Remy, Ursula
CORPORATE SOURCE: Federal Institute for Risk Assessment, Berlin, 14195, Germany
SOURCE: Toxicology (2005), 206(1), 33-48
CODEN: TXCYAC; ISSN: 0300-483X
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) is an ubiquitously distributed environmental pollutant. Health effects have been studied intensively, but low-dose effects are quite complex and not yet fully understood. In many studies, the immune system was identified as the most sensitive target. Here, we demonstrate changes of **protein** expression in liver and thymus of male marmosets (Callithrix jacchus) which were subjected to a single dose of a s.c. injection of 100 ng/kg body weight TCDD. Histopathol. examination revealed myocardial fibrosis, but there were no significant findings in pathol. and histopathol. of liver and thymus. In order to detect more subtle treatment-related changes, we performed a comparative proteomic investigation of liver and thymus using a 2-D gel electrophoresis based proteomics approach. Fluorescence labeling and automated image anal. was used to enhance sensitivity and reproducibility. In both organs, distinct changes of **protein** expression were detected which were more pronounced in thymus, where the pattern of deregulated **proteins** could be clearly related to immune responses. In the thymus of treated animals, several toxicol. relevant factors were increased, including chaperones, glycerol-3-phosphate dehydrogenase, and adseverin. Among others, vimentin, Ca-dependent protease and **protein** disulfide isomerase were downregulated. In the liver, transferrins, lamin A and HSP70 were upregulated, whereas thymidine phosphorylase (synonyms: endothelial cell growth factor, PD-ECGF, gliostatin) was significantly reduced. Comparative anal. of deregulated **proteins** in both organs revealed a pattern of related functions, which fits well into the existing knowledge of the toxic processes and mechanisms underlying TCDD-mediated toxicity.

REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:1029346 CAPLUS

DOCUMENT NUMBER: 142:110541

TITLE: Proteomic analysis of the response of Arabidopsis chloroplast **proteins** to high light stress

AUTHOR(S): Phee, Bong-Kwan; Cho, Jin-Hwan; Park, Sebyul; Jung, Jin Hee; Lee, Youn-Hyung; Jeon, Jong-Seong; Bhoo, Seong Hee; Hahn, Tae-Ryong

CORPORATE SOURCE: Graduate School of Biotechnology and Plant Metabolism Research Center, Kyung Hee University, Suwon, S. Korea

SOURCE: Proteomics (2004), 4(11), 3560-3568

CODEN: PROTC7; ISSN: 1615-9853

PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Light is an essential environmental factor in the progression of plant growth and development but prolonged exposure to high levels of light stress can cause cellular damage and ultimately result in the death of the plant. Plants can respond defensively to this stress for a limited period and this involves changes to their gene expression profiles. Proteomic approaches were therefore applied to the study of the response to high light stress in the Arabidopsis thaliana plant species. Wild-type Arabidopsis was grown under normal light (100 $\mu\text{mol photons}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) conditions and then subjected to high light (1000 $\mu\text{mol photons}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) stress. Chloroplasts were then isolated from these plants and both soluble and insol. **proteins** were extracted and subjected to two-dimensional (2-D) gel electrophoresis. The resolved **proteins** were subsequently identified by matrix assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS) and comparative database anal. 64 **Protein** spots, which were identified as candidate factors that responded to high light stress, were then selected for anal. and 52 of these were successfully identified using MALDI-TOF-MS anal. 35 Of the 52 identified **proteins** were found to decrease their expression levels during high light stress and a further 14 of the candidate **proteins** had upregulated expression levels under these conditions. Most of the **proteins** that were downregulated during high light stress are involved in photosynthesis pathways. However, many of the 14 upregulated **proteins** were identified as previously well-known high light stress-related **proteins**, such as heat shock **proteins** (HSPs), dehydroascorbate reductase (DHAR), and superoxide dismutase (SOD). Three novel **proteins** that were more highly expressed during periods of high light stress but had no clear functional relationship to these conditions, were also identified in this study.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:1013025 CAPLUS

DOCUMENT NUMBER: 142:20704

TITLE: Localization of the chaperone **proteins** GRP78 and HSP60 on the luminal surface of bovine oviduct epithelial cells and their association with spermatozoa

AUTHOR(S): Boillard, M.; Reyes-Moreno, C.; Lachance, C.; Massicotte, L.; Bailey, J. L.; Sirard, M.-A.; Leclerc, P.

CORPORATE SOURCE: Departement des Sciences Animales, Centre de Recherche en Biologie de la Reproduction, Universite Laval, Quebec, QC, G1K 7P4, Can.

SOURCE: Biology of Reproduction (2004), 71(6), 1879-1889
CODEN: BIREBV; ISSN: 0006-3363
PUBLISHER: Society for the Study of Reproduction
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Upon their transit through the female genital tract, bovine spermatozoa bind to oviduct epithelial cells, where they are maintained alive for long periods of time until fertilization. Although carbohydrate components of the oviduct epithelial cell membrane are involved in these sperm/oviduct interactions, no **protein** candidate has been identified to play this role. To identify the oviduct factors involved in their survival, sperm cells were preincubated for 30 min with apical membranes isolated from oviduct epithelial cells, washed extensively, and further incubated for up to 12 h in the absence of apical membranes. During this incubation, sperm viability, motility, and acrosomal integrity were improved compared with cells preincubated in the absence of apical membranes. This suggests that, during the 30-min preincubation with apical membrane exts., either an oviductal factor triggered intracellular events resulting in pos. effects on spermatozoa or that such a factor strongly attached to sperm cells to promote a pos. action. Similarly, spermatozoa were incubated with apical membranes isolated from oviduct epithelial cells labeled with [35S]-methionine and, upon extensive washes, **proteins** were separated by two-dimensional (2-D) **gel** electrophoresis to identify the factors suspected to have beneficial effects on spermatozoa. The six major **proteins**, according to their signal intensity on the autoradiog. film, were extracted from a 2-D **gel** of oviduct epithelial cell **proteins** run in parallel and processed for N-terminal sequencing of the first 15 amino acids. Of these, one was identical to heat shock **protein** 60 (HSP60) and one to the glucose-regulated **protein** 78 (GRP78). Their identities and association with spermatozoa were confirmed using an antibody directed against these **proteins**. This paper reports the localization of both GRP78 and HSP60 on the luminal/apical surface of oviduct epithelial cells, their binding to spermatozoa, and the presence of endogenous HSP60 in the sperm midpiece.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:767842 CAPLUS
DOCUMENT NUMBER: 142:357
TITLE: Proteomic analysis of **proteins** altered by dibenzoylmethane in human prostatic cancer LNCaP cells
AUTHOR(S): Frazier, Monica C.; Jackson, Kimberly M.; Jankowska-Stephens, Ewa; Anderson, Mark G.; Harris, Wayne B.
CORPORATE SOURCE: CBR/RCMI and Cancer Center, Tuskegee University, Tuskegee, AL, USA
SOURCE: Proteomics (2004), 4(9), 2814-2821
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This paper explores the use of proteomics as a tool for identifying **protein** species whose expression has been altered by dibenzoylmethane (DBM) in LNCaP cells. Although DBM, a constituent of licorice, has been shown to induce cell cycle arrest and regulate androgen receptor (AR) expression, the mechanism by which these events occur is unknown. To develop a better understanding of the effect of DBM on cancer cells, the authors analyzed changes in **protein** expression induced by DBM in LNCaP cells using two-dimensional (2-D) **gel** electrophoresis. The proteomic approach used to study LNCaP cells has lead to the anal. and identification of a number of **protein** species that increase or decrease as a result of exposure to DBM. In

particular, twenty features were differentially expressed in this study based on the quantitation of two sep. 2-D-fluorescence difference gel electrophoresis analyses. Thirteen of these features were identified through mass spectrometric anal. The intensity of 10 out of the 13 spots identified increased 2- to 3-fold in response to 25 μ M and 50 μ M DBM and the remaining three spots decreased 2-fold in response to the same DBM treatment. This study investigates proteomic changes induced by treatment of cells with DBM to develop a model for the mechanism by which DBM induces cell cycle arrest and represses AR expression.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:637204 CAPLUS

DOCUMENT NUMBER: 141:256616

TITLE: Differential proteomic analysis of intestinal epithelium cell line before and after irradiation by gamma-ray

AUTHOR(S): Zhang, Bo; Su, Yongping; Ai, Guoping; Liu, Xiaohong; Wei, Yongjiang; Wang, Fengchao; Cheng, Tianmin

CORPORATE SOURCE: College of Preventive Medicine, Third Military Medical University, Chongqing, 400038, Peop. Rep. China

SOURCE: Di-San Junyi Daxue Xuebao (2003), 25(24), 2157-2160
CODEN: DYXUE8; ISSN: 1000-5404

PUBLISHER: Di-San Junyi Daxue Xuebao Bianjibu

DOCUMENT TYPE: Journal

LANGUAGE: Chinese

AB Study the **proteins** associated with ionizing irradiation of intestinal epithelium cell line (IEC-6), and elucidate the mol. mechanism of reconstruction of intestinal epithelium damaged by ionizing irradiation **Protein** samples extracted from normal IEC-6 cells and IEC-6 cells irradiated by γ -ray at the dose of 25 Gy were separated by immobilized pH gradient two-dimensional (2-D) gel electrophoresis. After Coomassie blue staining, the 2-D electrophoretogram was analyzed using PDQuest software. The differential **proteins** were cut off from the Coomassie-blue stained gel and digested in gel with trypsin, and then identified by peptide mass fingerprinting based on matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF-MS) and database searching. Total RNA of IEC-6 cells was isolated and RT-PCR anal. was performed using primers of ERP29 and GAPDH. After Coomassie blue staining, the 2-DE image anal. by PDQuest software detected (608 \pm 39) spots in normal IEC-6 cell sample and (595 \pm 31) spots in irradiated cells, of which 396 spots were matched. Sixteen differential spots were cut off from the Coomassie blue stained gel, and 11 spots were preliminarily identified. These **proteins** were associated with cell metabolism, cytoskeleton, and free radical elimination, etc.

Ionizing radiation induced mRNA of ERP29 in a time-dependent manner over a 48-h period. The results indicated that γ -ray irradiation can induce changes of the **protein** expression pattern of intestinal epithelium cell line. This helps to understand the mol. mechanisms of ionizing radiation on intestinal epithelium cells.

L7 ANSWER 7 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:579538 CAPLUS

DOCUMENT NUMBER: 141:222844

TITLE: Heat shock **protein** 70 (Hsp70) subtype expression in neuroendocrine tissue and identification of a neuroendocrine tumour-specific Hsp70 truncation

AUTHOR(S): Zierhut, B.; Mechtler, K.; Gartner, W.; Daneva, T.; Base, W.; Weissel, M.; Niederle, B.; Wagner, L.

CORPORATE SOURCE: Department of Medicine III, Division of Clinical Endocrinology and Metabolism, University of Vienna, Vienna, A-1090, Austria

SOURCE: Endocrine-Related Cancer (2004), 11(2), 377-389
CODEN: ERCAE9; ISSN: 1351-0088
PUBLISHER: Society for Endocrinology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In order to identify neuroendocrine tumor-specific **protein** expression, we generated monoclonal antibodies (mAbs) with a tumor-related reaction pattern using a human insulinoma as immunogen. One of the generated mAbs (mAb 1D4) exhibited striking immunoreactivity against various neuroendocrine tumors without staining pancreatic islets of Langerhans. Furthermore, mAb 1D4 immunostained a characteristic subtype of hypothalamic neurons. Using two-dimensional (2-D) **gel** electrophoresis, mAb 1D4 immunoblotting and mass spectrometry, heat shock **protein** 70 (Hsp70) isoforms were identified as the mAb 1D4-specific antigen. In hypothalamic tissue, the presence of two different Hsp70 isoforms (Hsp70-8 and Hsp70-1) was revealed by 2-D **gel** immunoblots and consecutive mass spectrometric peptide anal. In contrast, insulinoma and other neuroendocrine tumors displayed solely Hsp70-8 expression. Moreover, the tumor-specific presence of an addnl. mAb 1D4 immunoreactive **protein** of 40 kDa was observed in eight out of eight tested neuroendocrine tumors. For this variant, exclusively, peptides derived from the C terminus excluding the 299 amino-terminal residues were detected. In cultured tumor-derived fibroblasts, expression of the truncated Hsp70-8 subtype was not present. In conclusion, we have demonstrated a neuroendocrine tumor-specific expression pattern of Hsp70 isoforms and identified an as yet unknown N-terminally truncated Hsp70-8 variant.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:576084 CAPLUS

DOCUMENT NUMBER: 141:257757

TITLE: The proteome of chicken skeletal muscle: Changes in soluble **protein** expression during growth in a layer strain

AUTHOR(S): Doherty, Mary K.; McLean, Lynn; Hayter, Julia R.; Pratt, Julie M.; Robertson, Duncan H. L.; El-Shafei, Abdel; Gaskell, Simon J.; Beynon, Robert J.

CORPORATE SOURCE: Protein Function Group, Department of Veterinary Preclinical Sciences, University of Liverpool, Liverpool, L69 7ZJ, UK

SOURCE: Proteomics (2004), 4(7), 2082-2093

CODEN: PROTC7; ISSN: 1615-9853

PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The whole animal, and the pectoralis muscle in particular, grows at a greatly enhanced rate in chickens selected for meat production (broilers) when compared to those selected for egg production (layers). As part of an ongoing study to analyze muscle **protein** dynamics under conditions of rapid growth, the authors have embarked upon a preliminary characterization of the proteome of layer chicken pectoralis muscle, at specified time-points from 1 to 27 days after hatching. Soluble exts. of muscle homogenates were separated by two-dimensional (2-D) **gel** electrophoresis and selected spots were analyzed by in-gel tryptic digestion and matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry. Of 90 spots, 51 gave mass spectra that matched to existing chicken **proteins** present in online databases, 12 matched equivalent **proteins** from non-avian species and 11 yielded good quality spectra but were unable to be matched against existing databases. For many of these **proteins**, growth over 27 days elicited dramatic changes in relative expression levels. Chicken skeletal muscle offers an excellent system for developmental proteomics.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:328454 CAPLUS

DOCUMENT NUMBER: 140:421867

TITLE: Nuclear matrix **protein** expressions in hepatocytes of normal and cirrhotic rat livers under normal and regenerating conditions

AUTHOR(S): Yun, Jing-Ping; Liew, Choong-Tsek; Chew, Eng Ching; Yin, Xiao-Yu; Lai, Paul Bo San; Fai, Yam Hin; Li, H. K. Richard; Jin, Mei-Lin; Ding, Ming-Xiao; Li, Ming-Tao; Lin, Han-Liang; Lau, Wan Yee

CORPORATE SOURCE: Department of Pathology, Cancer Center of Sun Yat-Sen University, Guangzhou, 510060, Peop. Rep. China

SOURCE: Journal of Cellular Biochemistry (2004), 91(6), 1269-1279

CODEN: JCEBD5; ISSN: 0730-2312

PUBLISHER: Wiley-Liss, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We explored the feasibility of studying nuclear matrix **protein** (NMP) expressions of the hepatocytes in normal and cirrhotic rat livers with liver regeneration after partial hepatectomy. Sixteen Wistar healthy rats were studied with exptl. liver regeneration and/or liver cirrhosis. Two-dimensional (2-D) **gel** electrophoresis was used to generate these NMP compns. from these rat liver samples. Several antibodies against cytokeratin, vimentin, actin, B23, HNF4alpha, and heat shock **protein** 70 were used for identification by Western blot. Totally, 41 strongly stained **protein** spots were characterized on the 2-D **gels**. Thirty-four **protein** spots were detected in all of these rat livers, of which, cytokeratin, vimentin, actin, HNF4alpha, and heat shock **protein** 70 were identified. B23 was detected in the regenerated livers. Three **protein** spots (s33, s34, and s35) were detectable only in NMP preparation extracted from the regenerating rat livers after hepatectomy. Another 3 **protein** spots (s36, s37, and s38) were detectable only in NMP preparation extracted from thioacetamide-induced cirrhotic rat livers. Under these conditions including exptl. liver regeneration and/or liver cirrhosis, Over thirty higher abundance NMPs of hepatocytes were consistently expressed and considered as common and basic NMPs. Some of the NMPs are specific for liver regeneration and may play a critical role in cell proliferation and cell cycle, and some are specific for liver cirrhosis.

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:161172 CAPLUS

DOCUMENT NUMBER: 140:284961

TITLE: F-actin capping (CapZ) and other contractile saphenous vein smooth muscle **proteins** are altered by hemodynamic stress: A proteomic approach

AUTHOR(S): McGregor, Emma; Kempster, Lee; Wait, Robin; Gosling, Martin; Dunn, Michael J.; Powell, Janet T.

CORPORATE SOURCE: Department of Vascular Surgery, Imperial College School of Medicine at Charing Cross Hospital, London, W6 8RP, UK

SOURCE: Molecular and Cellular Proteomics (2004), 3(2), 115-124

CODEN: MCPOBS; ISSN: 1535-9476

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Increased force generation and smooth muscle remodeling follow the implantation of saphenous vein as an arterial bypass graft. Previously, we characterized and mapped 129 **proteins** in human saphenous vein medial smooth muscle using two-dimensional (2-D) PAGE and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Here, we focus on actin filament remodeling in response to simulated arterial flow. Human saphenous vein was exposed to simulated venous or arterial flow for 90 min in vitro, and the contractile medial smooth muscle was dissected out and subjected to 2-D **gel** electrophoresis using a non-linear immobilized pH 3-10 gradient in the first dimension. **Proteins** were analyzed quant. using PDQuest 2-D software. The actin polymerization inhibitor cytochalasin B (1 μ M) prevented increases in force generation after 90 min of simulated arterial flow. At this time point, there were several consistent changes in actin filament-associated **protein** expression (seven paired vein samples). The heat shock **protein** HSP27, identified as a three-spot charge train, showed a 1.6-fold increase in abundance ($p = 0.01$), but with reduced representation of the phosphorylated Ser82 and Ser15Ser82 isoforms ($p = 0.018$). The abundance of actin-capping **protein** α 2 subunit CapZ had decreased 3-fold, $p = 0.04$. A 19-kDa proteolytic fragment of actin increased 2-fold, $p = 0.04$. For the four-spot charge train of gelsolin, there was reduced representation of the more acidic isoforms, $p = 0.022$. The abundance of other **proteins** associated with actin filaments, including cofilin and destrin, remained unchanged after arterial flow. Actin filament remodeling with differential expression and/or post-translational modification of **proteins** involved in capping the barbed end of actin filaments, HSP27 and CapZ, is an early response of contractile saphenous vein smooth muscle cells to hemodynamic stress. The observed changes would favor the generation of contractile stress fibers.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

(FILE 'HOME' ENTERED AT 13:31:18 ON 06 APR 2005)

FILE 'CAPLUS' ENTERED AT 13:31:28 ON 06 APR 2005

L1 1052 S @-D GEL
L2 0 S HEAT SKOCK PROTEINS
L3 0 S HEAT SKOCK PROTEIN
L4 0 S CHAPAERONE
L5 15629 S HSP
L6 42 S L1 AND L5
L7 42 S L6 AND PROTEIN
L8 0 S L7 AND PREVENTION AND DENATURATION
L9 0 S L7 AND PREVENTION

=> d L7 1-20 ibib,abs

L7 ANSWER 1 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:133528 CAPLUS
DOCUMENT NUMBER: 142:238591
TITLE: Proteomic profiling of human stem cells derived from umbilical cord blood
AUTHOR(S): Zenzmaier, Christoph; Gesslbauer, Bernd; Grobuschek, Nina; Jandrositz, Anita; Preisegger, Karl-Heinz; Kungl, Andreas J.
CORPORATE SOURCE: Lifecord Inc., Graz, A-8010, Austria
SOURCE: Biochemical and Biophysical Research Communications (2005), 328(4), 968-972
CODEN: BBRC A9; ISSN: 0006-291X
PUBLISHER: Elsevier

DOCUMENT TYPE: Journal
LANGUAGE: English
AB CD34+ preps. from five different umbilical cord samples were compared with respect to their proteome profile using 2-D gel electrophoresis. Fifty-two **protein** spots were found to match in all preps. referring to the high heterogeneity of such samples indicating a not fully developed (or instable) proteome of stem cells. All matching spots were subjected to in-gel digestion and nano-LC-MS/MS sequence anal., from which 22 **proteins** were unambiguously identified.
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1067027 CAPLUS
TITLE: Differential signatures of **protein** expression in marmoset liver and thymus induced by single-dose TCDD treatment
AUTHOR(S): Oberemm, Axel; Meckert, Christine; Brandenburger, Linda; Herzig, Andrea; Lindner, Yvonne; Kalenberg, Kareen; Krause, Eberhard; Ittrich, Carina; Kopp-Schneider, Annette; Stahlmann, Ralf; Richter-Reichhelm, Hans-Bernhard; Gundert-Remy, Ursula
CORPORATE SOURCE: Federal Institute for Risk Assessment, Berlin, 14195, Germany
SOURCE: Toxicology (2005), 206(1), 33-48
CODEN: TXCYAC; ISSN: 0300-483X
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) is an ubiquitously distributed environmental pollutant. Health effects have been studied intensively, but low-dose effects are quite complex and not yet fully understood. In many studies, the immune system was identified as the most sensitive target. Here, we demonstrate changes of **protein** expression in liver and thymus of male marmosets (Callithrix jacchus) which were subjected to a single dose of a s.c. injection of 100 ng/kg body weight TCDD. Histopathol. examination revealed myocardial fibrosis, but there were no significant findings in pathol. and histopathol. of liver and thymus. In order to detect more subtle treatment-related changes, we performed a comparative proteomic investigation of liver and thymus using a 2-D gel electrophoresis based proteomics approach. Fluorescence labeling and automated image anal. was used to enhance sensitivity and reproducibility. In both organs, distinct changes of **protein** expression were detected which were more pronounced in thymus, where the pattern of deregulated **proteins** could be clearly related to immune responses. In the thymus of treated animals, several toxicol. relevant factors were increased, including chaperones, glycerol-3-phosphate dehydrogenase, and adseverin. Among others, vimentin, Ca-dependent protease and **protein** disulfide isomerase were downregulated. In the liver, transferrins, lamin A and HSP70 were upregulated, whereas thymidine phosphorylase (synonyms: endothelial cell growth factor, PD-ECGF, gliostatin) was significantly reduced. Comparative anal. of deregulated **proteins** in both organs revealed a pattern of related functions, which fits well into the existing knowledge of the toxic processes and mechanisms underlying TCDD-mediated toxicity.
REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1029346 CAPLUS
DOCUMENT NUMBER: 142:110541
TITLE: Proteomic analysis of the response of Arabidopsis chloroplast **proteins** to high light stress

AUTHOR(S) : Phee, Bong-Kwan; Cho, Jin-Hwan; Park, Sebyul; Jung, Jin Hee; Lee, Youn-Hyung; Jeon, Jong-Seong; Bhoo, Seong Hee; Hahn, Tae-Ryong
CORPORATE SOURCE: Graduate School of Biotechnology and Plant Metabolism Research Center, Kyung Hee University, Suwon, S. Korea
SOURCE: Proteomics (2004), 4(11), 3560-3568
CODEN: PROTC7; ISSN: 1615-9853
PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Light is an essential environmental factor in the progression of plant growth and development but prolonged exposure to high levels of light stress can cause cellular damage and ultimately result in the death of the plant. Plants can respond defensively to this stress for a limited period and this involves changes to their gene expression profiles. Proteomic approaches were therefore applied to the study of the response to high light stress in the Arabidopsis thaliana plant species. Wild-type Arabidopsis was grown under normal light (100 $\mu\text{mol photons}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) conditions and then subjected to high light (1000 $\mu\text{mol photons}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) stress. Chloroplasts were then isolated from these plants and both soluble and insol. **proteins** were extracted and subjected to two-dimensional (2-D) **gel** electrophoresis. The resolved **proteins** were subsequently identified by matrix assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS) and comparative database anal. 64 **Protein** spots, which were identified as candidate factors that responded to high light stress, were then selected for anal. and 52 of these were successfully identified using MALDI-TOF-MS anal. 35 Of the 52 identified **proteins** were found to decrease their expression levels during high light stress and a further 14 of the candidate **proteins** had upregulated expression levels under these conditions. Most of the **proteins** that were downregulated during high light stress are involved in photosynthesis pathways. However, many of the 14 upregulated **proteins** were identified as previously well-known high light stress-related **proteins**, such as heat shock **proteins** (HSPs), dehydroascorbate reductase (DHAR), and superoxide dismutase (SOD). Three novel **proteins** that were more highly expressed during periods of high light stress but had no clear functional relationship to these conditions, were also identified in this study.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:1013025 CAPLUS
DOCUMENT NUMBER: 142:20704
TITLE: Localization of the chaperone **proteins** GRP78 and HSP60 on the luminal surface of bovine oviduct epithelial cells and their association with spermatozoa
AUTHOR(S) : Boilard, M.; Reyes-Moreno, C.; Lachance, C.; Massicotte, L.; Bailey, J. L.; Sirard, M.-A.; Leclerc, P.
CORPORATE SOURCE: Departement des Sciences Animales, Centre de Recherche en Biologie de la Reproduction, Universite Laval, Quebec, QC, G1K 7P4, Can.
SOURCE: Biology of Reproduction (2004), 71(6), 1879-1889
CODEN: BIREBV; ISSN: 0006-3363
PUBLISHER: Society for the Study of Reproduction
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Upon their transit through the female genital tract, bovine spermatozoa bind to oviduct epithelial cells, where they are maintained alive for long periods of time until fertilization. Although carbohydrate components of

the oviduct epithelial cell membrane are involved in these sperm/oviduct interactions, no **protein** candidate has been identified to play this role. To identify the oviduct factors involved in their survival, sperm cells were preincubated for 30 min with apical membranes isolated from oviduct epithelial cells, washed extensively, and further incubated for up to 12 h in the absence of apical membranes. During this incubation, sperm viability, motility, and acrosomal integrity were improved compared with cells preincubated in the absence of apical membranes. This suggests that, during the 30-min preincubation with apical membrane exts., either an oviductal factor triggered intracellular events resulting in pos. effects on spermatozoa or that such a factor strongly attached to sperm cells to promote a pos. action. Similarly, spermatozoa were incubated with apical membranes isolated from oviduct epithelial cells labeled with [35S]-methionine and, upon extensive washes, **proteins** were separated by two-dimensional (2-D) **gel** electrophoresis to identify the factors suspected to have beneficial effects on spermatozoa. The six major **proteins**, according to their signal intensity on the autoradiog. film, were extracted from a 2-D **gel** of oviduct epithelial cell **proteins** run in parallel and processed for N-terminal sequencing of the first 15 amino acids. Of these, one was identical to heat shock **protein** 60 (HSP60) and one to the glucose-regulated **protein** 78 (GRP78). Their identities and association with spermatozoa were confirmed using an antibody directed against these **proteins**. This paper reports the localization of both GRP78 and HSP60 on the luminal/apical surface of oviduct epithelial cells, their binding to spermatozoa, and the presence of endogenous HSP60 in the sperm midpiece.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:767842 CAPLUS

DOCUMENT NUMBER: 142:357

TITLE: Proteomic analysis of **proteins** altered by dibenzoylmethane in human prostatic cancer LNCaP cells
AUTHOR(S): Frazier, Monica C.; Jackson, Kimberly M.; Jankowska-Stephens, Ewa; Anderson, Mark G.; Harris, Wayne B.

CORPORATE SOURCE: CBR/RCMI and Cancer Center, Tuskegee University, Tuskegee, AL, USA

SOURCE: Proteomics (2004), 4(9), 2814-2821

CODEN: PROTC7; ISSN: 1615-9853

PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA

DOCUMENT TYPE: Journal

LANGUAGE: English

AB This paper explores the use of proteomics as a tool for identifying **protein** species whose expression has been altered by dibenzoylmethane (DBM) in LNCaP cells. Although DBM, a constituent of licorice, has been shown to induce cell cycle arrest and regulate androgen receptor (AR) expression, the mechanism by which these events occur is unknown. To develop a better understanding of the effect of DBM on cancer cells, the authors analyzed changes in **protein** expression induced by DBM in LNCaP cells using two-dimensional (2-D) **gel** electrophoresis. The proteomic approach used to study LNCaP cells has lead to the anal. and identification of a number of **protein** species that increase or decrease as a result of exposure to DBM. In particular, twenty features were differentially expressed in this study based on the quantitation of two sep. 2-D-fluorescence difference gel electrophoresis analyses. Thirteen of these features were identified through mass spectrometric anal. The intensity of 10 out of the 13 spots identified increased 2- to 3-fold in response to 25 μ M and 50 μ M DBM and the remaining three spots decreased 2-fold in response to the same DBM treatment. This study investigates proteomic changes induced by treatment of cells with DBM to develop a model for the mechanism by which DBM

induces cell cycle arrest and represses AR expression.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:637204 CAPLUS

DOCUMENT NUMBER: 141:256616

TITLE: Differential proteomic analysis of intestinal epithelium cell line before and after irradiation by gamma-ray

AUTHOR(S): Zhang, Bo; Su, Yongping; Ai, Guoping; Liu, Xiaohong; Wei, Yongjiang; Wang, Fengchao; Cheng, Tianmin

CORPORATE SOURCE: College of Preventive Medicine, Third Military Medical University, Chongqing, 400038, Peop. Rep. China

SOURCE: Di-San Junyi Daxue Xuebao (2003), 25(24), 2157-2160
CODEN: DYXUE8; ISSN: 1000-5404

PUBLISHER: Di-San Junyi Daxue Xuebao Bianjibu

DOCUMENT TYPE: Journal

LANGUAGE: Chinese

AB Study the **proteins** associated with ionizing irradiation of intestinal epithelium cell line (IEC-6), and elucidate the mol. mechanism of reconstruction of intestinal epithelium damaged by ionizing irradiation. **Protein** samples extracted from normal IEC-6 cells and IEC-6 cells irradiated by γ -ray at the dose of 25 Gy were separated by immobilized pH gradient two-dimensional (2-D) gel electrophoresis. After Coomassie blue staining, the 2-D electrophoretogram was analyzed using PDQuest software. The differential **proteins** were cut off from the Coomassie-blue stained gel and digested in gel with trypsin, and then identified by peptide mass fingerprinting based on matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF-MS) and database searching. Total RNA of IEC-6 cells was isolated and RT-PCR anal. was performed using primers of ERP29 and GAPDH. After Coomassie blue staining, the 2-DE image anal. by PDQuest software detected (608 \pm 39) spots in normal IEC-6 cell sample and (595 \pm 31) spots in irradiated cells, of which 396 spots were matched. Sixteen differential spots were cut off from the Coomassie blue stained gel, and 11 spots were preliminarily identified. These **proteins** were associated with cell metabolism, cytoskeleton, and free radical elimination, etc.

Ionizing radiation induced mRNA of ERP29 in a time-dependent manner over a 48-h period. The results indicated that γ -ray irradiation can induce changes of the **protein** expression pattern of intestinal epithelium cell line. This helps to understand the mol. mechanisms of ionizing radiation on intestinal epithelium cells.

L7 ANSWER 7 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:579538 CAPLUS

DOCUMENT NUMBER: 141:222844

TITLE: Heat shock **protein** 70 (Hsp70) subtype expression in neuroendocrine tissue and identification of a neuroendocrine tumour-specific Hsp70 truncation

AUTHOR(S): Zierhut, B.; Mechtler, K.; Gartner, W.; Daneva, T.; Base, W.; Weissel, M.; Niederle, B.; Wagner, L.

CORPORATE SOURCE: Department of Medicine III, Division of Clinical Endocrinology and Metabolism, University of Vienna, Vienna, A-1090, Austria

SOURCE: Endocrine-Related Cancer (2004), 11(2), 377-389
CODEN: ERCAE9; ISSN: 1351-0088

PUBLISHER: Society for Endocrinology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In order to identify neuroendocrine tumor-specific **protein** expression, we generated monoclonal antibodies (mAbs) with a tumor-related reaction pattern using a human insulinoma as immunogen. One of the

generated mAbs (mAb 1D4) exhibited striking immunoreactivity against various neuroendocrine tumors without staining pancreatic islets of Langerhans. Furthermore, mAb 1D4 immunostained a characteristic subtype of hypothalamic neurons. Using two-dimensional (2-D) gel electrophoresis, mAb 1D4 immunoblotting and mass spectrometry, heat shock protein 70 (Hsp70) isoforms were identified as the mAb 1D4-specific antigen. In hypothalamic tissue, the presence of two different Hsp70 isoforms (Hsp70-8 and Hsp70-1) was revealed by 2-D gel immunoblots and consecutive mass spectrometric peptide anal. In contrast, insulinoma and other neuroendocrine tumors displayed solely Hsp70-8 expression. Moreover, the tumor-specific presence of an addnl. mAb 1D4 immunoreactive protein of 40 kDa was observed in eight out of eight tested neuroendocrine tumors. For this variant, exclusively, peptides derived from the C terminus excluding the 299 amino-terminal residues were detected. In cultured tumor-derived fibroblasts, expression of the truncated Hsp70-8 subtype was not present. In conclusion, we have demonstrated a neuroendocrine tumor-specific expression pattern of Hsp70 isoforms and identified an as yet unknown N-terminally truncated Hsp70-8 variant.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:576084 CAPLUS

DOCUMENT NUMBER: 141:257757

TITLE: The proteome of chicken skeletal muscle: Changes in soluble protein expression during growth in a layer strain

AUTHOR(S): Doherty, Mary K.; McLean, Lynn; Hayter, Julia R.; Pratt, Julie M.; Robertson, Duncan H. L.; El-Shafei, Abdel; Gaskell, Simon J.; Beynon, Robert J.

CORPORATE SOURCE: Protein Function Group, Department of Veterinary Preclinical Sciences, University of Liverpool, Liverpool, L69 7ZJ, UK

SOURCE: Proteomics (2004), 4(7), 2082-2093

CODEN: PROTC7; ISSN: 1615-9853

PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The whole animal, and the pectoralis muscle in particular, grows at a greatly enhanced rate in chickens selected for meat production (broilers) when compared to those selected for egg production (layers). As part of an ongoing study to analyze muscle protein dynamics under conditions of rapid growth, the authors have embarked upon a preliminary characterization of the proteome of layer chicken pectoralis muscle, at specified time-points from 1 to 27 days after hatching. Soluble exts. of muscle homogenates were separated by two-dimensional (2-D) gel electrophoresis and selected spots were analyzed by in-gel tryptic digestion and matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry. Of 90 spots, 51 gave mass spectra that matched to existing chicken proteins present in online databases, 12 matched equivalent proteins from non-avian species and 11 yielded good quality spectra but were unable to be matched against existing databases. For many of these proteins, growth over 27 days elicited dramatic changes in relative expression levels. Chicken skeletal muscle offers an excellent system for developmental proteomics.

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L7 ANSWER 9 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:328454 CAPLUS

DOCUMENT NUMBER: 140:421867

TITLE: Nuclear matrix protein expressions in hepatocytes of normal and cirrhotic rat livers under

normal and regenerating conditions
AUTHOR(S): Yun, Jing-Ping; Liew, Choong-Tsek; Chew, Eng Ching;
Yin, Xiao-Yu; Lai, Paul Bo San; Fai, Yam Hin; Li, H.
K. Richard; Jin, Mei-Lin; Ding, Ming-Xiao; Li,
Ming-Tao; Lin, Han-Liang; Lau, Wan Yee
CORPORATE SOURCE: Department of Pathology, Cancer Center of Sun Yat-Sen
University, Guangzhou, 510060, Peop. Rep. China
SOURCE: Journal of Cellular Biochemistry (2004), 91(6),
1269-1279
CODEN: JCEBD5; ISSN: 0730-2312
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We explored the feasibility of studying nuclear matrix **protein**
(NMP) expressions of the hepatocytes in normal and cirrhotic rat livers
with liver regeneration after partial hepatectomy. Sixteen Wistar healthy
rats were studied with exptl. liver regeneration and/or liver cirrhosis.
Two-dimensional (2-D) **gel** electrophoresis was used to
generate these NMP comps. from these rat liver samples. Several
antibodies against cytokeratin, vimentin, actin, B23, HNF4alpha, and heat
shock **protein** 70 were used for identification by Western blot.
Totally, 41 strongly stained **protein** spots were characterized on
the 2-D **gels**. Thirty-four **protein** spots
were detected in all of these rat livers, of which, cytokeratin, vimentin,
actin, HNF4alpha, and heat shock **protein** 70 were identified.
B23 was detected in the regenerated livers. Three **protein** spots
(s33, s34, and s35) were detectable only in NMP preparation extracted from the
regenerating rat livers after hepatectomy. Another 3 **protein**
spots (s36, s37, and s38) were detectable only in NMP preparation extracted
from
thioacetamide-induced cirrhotic rat livers. Under these conditions
including exptl. liver regeneration and/or liver cirrhosis, Over thirty
higher abundance NMPs of hepatocytes were consistently expressed and
considered as common and basic NMPs. Some of the NMPs are specific for
liver regeneration and may play a critical role in cell proliferation and
cell cycle, and some are specific for liver cirrhosis.

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:161172 CAPLUS
DOCUMENT NUMBER: 140:284961
TITLE: F-actin capping (CapZ) and other contractile saphenous
vein smooth muscle **proteins** are altered by
hemodynamic stress: A proteomic approach
AUTHOR(S): McGregor, Emma; Kempster, Lee; Wait, Robin; Gosling,
Martin; Dunn, Michael J.; Powell, Janet T.
CORPORATE SOURCE: Department of Vascular Surgery, Imperial College
School of Medicine at Charing Cross Hospital, London,
W6 8RP, UK
SOURCE: Molecular and Cellular Proteomics (2004), 3(2),
115-124
CODEN: MCPOBS; ISSN: 1535-9476
PUBLISHER: American Society for Biochemistry and Molecular
Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Increased force generation and smooth muscle remodeling follow the
implantation of saphenous vein as an arterial bypass graft. Previously,
we characterized and mapped 129 **proteins** in human saphenous vein
medial smooth muscle using two-dimensional (2-D) PAGE and matrix-assisted
laser desorption/ionization time-of-flight mass spectrometry. Here, we
focus on actin filament remodeling in response to simulated arterial flow.
Human saphenous vein was exposed to simulated venous or arterial flow for

90 min in vitro, and the contractile medial smooth muscle was dissected out and subjected to 2-D gel electrophoresis using a non-linear immobilized pH 3-10 gradient in the first dimension. **Proteins** were analyzed quant. using PDQuest 2-D software. The actin polymerization inhibitor cytochalasin B (1 μ M) prevented increases in force generation after 90 min of simulated arterial flow. At this time point, there were several consistent changes in actin filament-associated **protein** expression (seven paired vein samples). The heat shock **protein** HSP27, identified as a three-spot charge train, showed a 1.6-fold increase in abundance ($p = 0.01$), but with reduced representation of the phosphorylated Ser82 and Ser15Ser82 isoforms ($p = 0.018$). The abundance of actin-capping **protein** $\alpha 2$ subunit CapZ had decreased 3-fold, $p = 0.04$. A 19-kDa proteolytic fragment of actin increased 2-fold, $p = 0.04$. For the four-spot charge train of gelsolin, there was reduced representation of the more acidic isoforms, $p = 0.022$. The abundance of other **proteins** associated with actin filaments, including cofilin and destrin, remained unchanged after arterial flow. Actin filament remodeling with differential expression and/or post-translational modification of **proteins** involved in capping the barbed end of actin filaments, HSP27 and CapZ, is an early response of contractile saphenous vein smooth muscle cells to hemodynamic stress. The observed changes would favor the generation of contractile stress fibers.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:73404 CAPLUS

DOCUMENT NUMBER: 140:332868

TITLE: Phosphoproteome Analysis of Cardiomyocytes Subjected to β -Adrenergic Stimulation. Identification and characterization of a cardiac heat shock **protein** p20

AUTHOR(S): Chu, Guoxiang; Egnaczyk, Gregory F.; Zhao, Wen; Jo, Su-Hyun; Fan, Guo-Chang; Maggio, John E.; Xiao, Rui-Ping; Kraniias, Evangelia G.

CORPORATE SOURCE: Department of Pharmacology & Cell Biophysics, University of Cincinnati College of Medicine, Cincinnati, OH, USA

SOURCE: Circulation Research (2004), 94(2), 184-193

CODEN: CIRUAL; ISSN: 0009-7330

PUBLISHER: Lippincott Williams & Wilkins

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Posttranslational modification of target substrates underlies biol. processes through activation/inactivation of signaling cascades. To concurrently identify the phosphoprotein substrates associated with cardiac β -adrenergic signaling, the mouse myocyte phosphoproteome was analyzed using 2-D gel electrophoresis in combination with 32 P autoradiog. Phosphoprotein spots, detected by silver staining, were identified using MALDI-TOF mass spectrometry in conjunction with computer-assisted **protein** spot matching. Stimulation with isoproterenol (1 μ mol/L for 5 min) was associated with maximal increases in myocyte contractile parameters, and significant stimulation of the phosphorylation of troponin I (190 \pm 23%) and succinyl CoA synthetase (160 \pm 16%), whereas the phosphorylation of pyruvate dehydrogenase (48 \pm 10%), NADH-ubiquinone oxidoreductase (46 \pm 6%), heat shock **protein** 27 (18 \pm 3%), α B-crystallin (20 \pm 3%), and an unidentified 26-kDa **protein** (29 \pm 7%) was significantly decreased, compared with unstimulated cells (100%). After sustained (30 min) stimulation with isoproterenol, only the alterations in the phosphorylation levels of troponin I and NADH-ubiquinone oxidoreductase were maintained and de novo phosphorylation of a phosphoprotein (\approx 20 kDa and pI 5.5) was observed. The tryptic peptide fragments of this phosphoprotein were sequenced using postsorce decay mass

spectrometry, and the **protein** was subsequently cloned and designated as p20, based on its high sequence homol. with rat and human skeletal p20. The mouse cardiac p20 contains the conserved domain sequences for heat shock **proteins**, and the RRAS consensus sequence for cAMP-PKA substrates. LC-MS/MS phosphorylation mapping confirmed phosphorylation of Ser16 in p20 on β -agonist stimulation. Adenoviral gene transfer of p20 was associated with significant increases in contractility and Ca transient peak in adult rat cardiomyocytes, suggesting an important role of p20 in cardiac function. These findings suggest that cardiomyocytes undergo significant posttranslational modification via phosphorylation in a multitude of **proteins** to dynamically fine-tune cardiac responses to β -adrenergic signaling.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 12 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:786668 CAPLUS

DOCUMENT NUMBER: 140:38508

TITLE: Surface localized heat shock **protein** 20 (HslV) of *Helicobacter pylori*

AUTHOR(S): Du, Rui Juan; Ho, Bow

CORPORATE SOURCE: Department of Microbiology, National University of Singapore, Singapore, 117597, Singapore

SOURCE: *Helicobacter* (2003), 8(4), 257-267

CODEN: HELIFL; ISSN: 1083-4389

PUBLISHER: Blackwell Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Heat Shock **Protein** (HSP) has been regarded as a pathogenic factor in *Helicobacter pylori* infection. Heat Shock **Protein** 20 (HSP20) of *H. pylori* is identified as HslV based on open reading frame predication of genome sequences. It is a homolog of HslV of *E. coli*, a peptidase involved in **protein** degradation. The HSP20 gene was cloned and inserted into pET16b fused with His-tag. Recombinant HSP20 **protein** (rHSP20) was expressed and purified by nickel column. Rabbit anti-rHSP20 was purified by **Protein A** affinity chromatog. and used as a probe to localize HSP20 in *H. pylori* by immuno-gold labeling and Western blotting. RHSP20 was also used as antigen to test for antibody against HSP20 in patients with *H. pylori* infection by ELISA. Immuno-gold labeled transmission electron microscopy shows that HSP20 is located on the cell surface of *H. pylori*. Western blotting of 2-D gel shows that HSP20 has a pI of .apprx.5.5 and a mol. weight of .apprx.18 kDa. The ELISA result shows that there is no significant difference in antibody titer against rHSP20 in all sera tested. The presence of IgG to rHSP20 may imply an earlier exposure of the patients and normal subjects to *H. pylori*. However, the mechanism has not been established. HSP20 has been shown to localize on the surface of *H. pylori*. Surface localization of *H. pylori* HSP20 may provide the path to a better understanding of the role and function of HSP20 in bacteria-host interaction.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:756715 CAPLUS

DOCUMENT NUMBER: 139:319795

TITLE: Developmentally induced changes of the proteome in the protozoan parasite *Leishmania donovani*

AUTHOR(S): Bente, Meike; Harder, Simone; Wiesgigl, Martina; Heukeshoven, Jochen; Gelhaus, Christoph; Krause, Eberhard; Clos, Joachim; Bruchhaus, Iris

CORPORATE SOURCE: Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany

SOURCE: *Proteomics* (2003), 3(9), 1811-1829

CODEN: PROTC7; ISSN: 1615-9853

PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In order to proceed through their life cycle, protozoan parasites of the genus *Leishmania* cycle between sandflies and mammals. This change of environment correlates with the differentiation from the promastigote stage (insect form) to the amastigote stage (intracellular mammalian form). The mol. basis underlying this major transformation is poorly understood so far; however, heat shock **protein 90** (HSP90) appears to play a pivotal role. To further elucidate this process we identified **proteins** expressed preferentially in either of the two life cycle stages. By using two-dimensional (2-D) **gel** electrophoresis we observed defined changes in the **protein** pattern. A total of approx. 2000 **protein** spots were visualized. Of these, 31 **proteins** were present only in promastigotes. The abundance of 65 **proteins** increased during heat-induced in vitro amastigote differentiation, while a decreased abundance is observed for four **proteins** late in amastigote differentiation. Further analyses using matrix-assisted laser desorption/ionization-time of flight mass spectrometry and peptide mass fingerprinting 67 **protein** spots were identified representing 41 different **proteins** known from databases and eight hypothetical **proteins**. Further studies showed that most of the stage-specific **proteins** fall into five groups of functionally related **proteins**. These functional categories are: (i) stress response (e.g. heat, oxidative stress); cytoskeleton and cell membrane; (iii) energy metabolism and phosphorylation; (iv) cell cycle and proliferation; and (v) amino acid metabolism. Very similar changes in the 2-D **protein** pattern were obtained when in vitro amastigote differentiation was induced either by pharmacol. inhibition of HSP90 or by a combination of heat stress and acidic pH supporting the critical role for HSP90 in life cycle control.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 14 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:187666 CAPLUS

DOCUMENT NUMBER: 138:352824

TITLE: Identification of cellular changes associated with increased production of human growth hormone in a recombinant chinese hamster ovary cell line

AUTHOR(S): Van Dyk, Derek D.; Misztal, David R.; Wilkins, Marc R.; Mackintosh, James A.; Poljak, Anne; Varnai, Jodie C.; Teber, Erdahl; Walsh, Bradley J.; Gray, Peter P.

CORPORATE SOURCE: Australian Proteome Analysis Facility, Macquarie University, Sydney, 2109, Australia

SOURCE: Proteomics (2003), 3(2), 147-156

CODEN: PROTC7; ISSN: 1615-9853

PUBLISHER: Wiley-VCH Verlag GmbH & Co. KGaA

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A proteomics approach was used to identify the **proteins** potentially implicated in the cellular response concomitant with elevated production levels of human growth hormone in a recombinant Chinese hamster ovary (CHO) cell line following exposure to 0.5 mM butyrate and 80 μ M zinc sulfate in the production media. This involved incorporation of two-dimensional (2-D) **gel** electrophoresis and **protein** identification by a combination of N-terminal sequencing, matrix-assisted laser desorption/ionization-time of flight mass spectrometry, amino acid anal. and cross species database matching. From these identifications a CHO 2-D reference map and annotated database have been established. Metabolic labeling and subsequent autoradiog. showed the induction of a number of cellular **proteins** in response to the media

additives butyrate and zinc sulfate. These were identified as GRP75, enolase and thioredoxin. The chaperone **proteins** GRP78, HSP90, GRP94 and HSP70 were not up-regulated under these conditions.

REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2002:102809 CAPLUS

DOCUMENT NUMBER: 136:212531

TITLE: Small heat shock **protein** p26 associates with nuclear lamins and HSP70 in nuclei and nuclear matrix fractions from stressed cells

AUTHOR(S): Willsie, Julia K.; Clegg, James S.

CORPORATE SOURCE: Section of Molecular and Cellular Biology, Bodega Marine Laboratory, University of California (Davis), Bodega Bay, CA, 94923, USA

SOURCE: Journal of Cellular Biochemistry (2001), 84(3), 601-614

CODEN: JCEBD5; ISSN: 0730-2312

PUBLISHER: Wiley-Liss, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The small heat shock/ α -crystallin **protein** p26 undergoes nuclear translocation in response to stress in encysted embryos of the brine shrimp *Artemia franciscana*. About 50% of total p26 translocates to nuclei in embryos treated with heat shock or anoxia, and in embryo homogenates incubated at low pH. Nuclear fractionation shows that the majority of nuclear p26 and a nuclear lamin are associated with the nuclear matrix fraction. To further explore the roles of p26 and other **HSPs** in stabilizing nuclear matrix **proteins** (NMPs), nuclear matrixes from control, and heat-shocked embryos were disassembled in urea and evaluated by one and two-dimensional (2-D) gel electrophoresis and Western immunoblotting after reassembling. Nuclear lamins were present only in reassembled fractions and, in the case of heat shock, p26 and HSP70 were also present. HSP90 was not detected in any nuclear fraction. Confocal microscopy on isolated nuclei and nuclear matrix preps. from control and heat-shocked embryos showed that the majority of p26 and a nuclear lamin share similar nuclear distributions. The combination of microscopy and fractionation results suggests that p26 and HSP70 play a role in the protection of nuclear lamins within the nuclear matrix.

REFERENCE COUNT: 101 THERE ARE 101 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 16 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:689424 CAPLUS

DOCUMENT NUMBER: 135:353186

TITLE: Proteome alterations in human hepatoma cells transfected with antisense epidermal growth factor receptor sequence

AUTHOR(S): Yu, Li-Rong; Shao, Xiao-Xia; Jiang, Wan-Li; Xu, Dan; Chang, Yun-Chao; Xu, Yong-Hua; Xia, Qi-Chang

CORPORATE SOURCE: Research Center for Proteome Institute of Biochemistry and Cell Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, 200031, Peop. Rep. China

SOURCE: Electrophoresis (2001), 22(14), 3001-3008

CODEN: ELCTDN; ISSN: 0173-0835

PUBLISHER: Wiley-VCH Verlag GmbH

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The epidermal growth factor (EGF) is a member of the growth factor superfamily that can stimulate the proliferation of many types of cells.

Overexpression of EGF receptor (EGFR) was observed in many types of cancer cells. Anti-EGFR antibodies or antisense nucleic acid sequences of EGFR can suppress the growth of hepatoma cells. In order to further investigate the proteome alterations associated with malignant growth of the human hepatoma cells and the influence of EGFR signal pathway on the cellular proteome, the authors have comparatively analyzed the proteomes of human hepatoma cells transfected with antisense EGFR sequence (cell strain JX-1) and its control cells (cell strain JX-0) by two-dimensional (2-D) gel electrophoresis and mass spectrometry.

Image anal. of silver-stained 2-D gels revealed that 40 **protein** spots showed significant expression changes in JX-1 cells compared to JX-0 cells. Three of them, including the tumor suppressor **protein** maspin, changed with tendency to the normal levels. Two **protein** spots were identified as HSP27 in the same gel, and one of them had a reduced level in JX-1 cells. The apparent alterations of HSP27 in expression level might be the results from their differential chemical modifications, suggesting the effect of dynamic post-translational modifications of **proteins** on the growth of hepatoma cells. Other **proteins** such as glutathione peroxidase (GPX-1) and 14-3-3-sigma also exhibited altered expression in JX-1 cells, and their functional implications are discussed.

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 17 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:527698 CAPLUS

DOCUMENT NUMBER: 136:180356

TITLE: Modification of the **protein** expression pattern induced in the nitrogen-fixing actinomycete *Frankia* sp. strain ACN14a-tsr by root exudates of its symbiotic host *Alnus glutinosa* and cloning of the *sodF* gene

AUTHOR(S): Hammad, Y.; Marechal, J.; Cournoyer, B.; Normand, P.; Domenach, A.-M.

CORPORATE SOURCE: Ecologie Microbienne. UMR CNRS 5557, Universite LYON 1, Villeurbanne, 69622, Fr.

SOURCE: Canadian Journal of Microbiology (2001), 47(6), 541-547

CODEN: CJMIAZ; ISSN: 0008-4166

PUBLISHER: National Research Council of Canada

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Two-dimensional (2-D) polyacrylamide gel electrophoresis was used to detect **proteins** induced in *Frankia* sp. strain ACN14a-tsr by root exudates of its symbiotic host, *Alnus glutinosa*. The 5 most prominent **proteins** were purified from 2-D gels and characterized by N-terminal sequencing. All of these **proteins** had a high percentage of similarity with known stress **proteins**. One **protein** match was the Fe superoxide dismutase (Fe-SOD), another was a tellurite resistance **protein** (Ter), the third was a bacterioferritin comigratory **protein** (Bcp): and two matches, differing only by their isoelec. point, were the same small heat shock **protein** (Hsp), a major immune reactive **protein** found in mycobacteria. This suggests that the symbiotic microorganism *Frankia*, first responds with a normal stress response to toxic root products of its symbiotic host plant. To confirm its identity, the gene corresponding to the Fe-SOD **protein**, *sodF* was isolated from a genomic library by a PCR-approach and sequenced. It is the first stress response gene characterized in *Frankia*.

REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 18 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:362017 CAPLUS

DOCUMENT NUMBER: 135:90969
 TITLE: The reduction of NADH ubiquinone oxidoreductase 24- and 75-kDa subunits in brains of patients with Down syndrome and Alzheimer's disease
 AUTHOR(S): Kim, Seong Hwan; Vlkolinsky, Roman; Cairns, Nigel; Fountoulakis, Michael; Lubec, Gert
 CORPORATE SOURCE: Department of Pediatrics, University of Vienna, Vienna, A-1090, Austria
 SOURCE: Life Sciences (2001), 68(24), 2741-2750
 CODEN: LIFSAK; ISSN: 0024-3205
 PUBLISHER: Elsevier Science Inc.
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB NADH:ubiquinone oxidoreductase (complex I), one of the most complicated multi-**protein** enzyme complexes, is important for energy metabolism because it is the initial enzyme of the mitochondrial respiratory chain. Deficiency of complex I is frequently found in various tissues of patients with neurodegenerative disease. Here we studied the **protein** levels of complex I 24- and 75-kDa subunits in several brain regions from patients with Down syndrome (DS) and Alzheimer's disease (AD). We determined **protein** levels of complex I 24-, 75-kDa subunits and mitochondrial marker **proteins** mitochondrial matrix **protein** P1 (hsp60) and aconitate hydratase from seven brain regions of patients with DS, AD and controls. **Proteins** were separated by two-dimensional (2-D) gel electrophoresis and identified by matrix-assisted laser desorption ionization mass spectrometry (MALDI-MS). Complex I 24-kDa subunit was significantly reduced in occipital cortex and thalamus in patients with DS and temporal and occipital cortices in patients with AD. Complex I 75-kDa subunit was significantly reduced in brain regions from patients with DS (temporal, occipital and caudate nucleus) and AD (parietal cortex). Redns. of two subunits of complex I may lead to the impairment of energy metabolism and result in neuronal cell death (apoptosis), a hallmark of both neurodegenerative disorders.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 19 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:659286 CAPLUS
 DOCUMENT NUMBER: 133:361412
 TITLE: Identification of differentially expressed **proteins** between human hepatoma and normal liver cell lines by two-dimensional electrophoresis and liquid chromatography-ion trap mass spectrometry
 AUTHOR(S): Yu, Li-Rong; Zeng, Rong; Shao, Xiao-Xia; Wang, Nan; Xu, Yong-Hua; Xia, Qi-Chang
 CORPORATE SOURCE: Shanghai Institute of Biochemistry, Chinese Academy of Sciences, Shanghai, 200031, Peop. Rep. China
 SOURCE: Electrophoresis (2000), 21(14), 3058-3068
 CODEN: ELCTDN; ISSN: 0173-0835
 PUBLISHER: Wiley-VCH Verlag GmbH
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB In the previous study, the proteomes of the human hepatoma cell line BEL-7404 and the normal human liver cell line L-02 were separated by high resolution two-dimensional electrophoresis (2-DE). Image anal. revealed that 99 **protein** spots showed quant. and qual. variations that were significant ($P < 0.01$) and reproducible. Here we report the identification results of some of these **protein** spots. **Protein** spots excised from 2-D gels were subjected to in-gel digestion with trypsin, and the resulting peptides were measured by microbore high performance liquid chromatog. - ion trap - mass spectrometry (LC-IT-MS) to obtain the tandem mass (MS/MS) spectra. Twelve **protein** spots were identified with high confidence using SEQUEST with uninterpreted MS/MS raw data. Besides inosine-5'-

monophosphate dehydrogenase 2, heat shock 27 kDa **protein**, calreticulin and calmodulin, whose expression was elevated in hepatoma cells, glutathione-S-transferase P was identified from hepatoma cells in which its level was 18-fold higher compared to human liver cells. Two spots were identified as the homologs of reticulocalbin for the first time in hepatoma cells and their expression increased compared to liver cells. However, tubulin beta-1 chain and natural killer cell enhancing factor B were downregulated in hepatoma cells. A tumor suppressing serpin, maspin precursor, was identified from one spot whose quantity was much higher in the normal liver cell line. More interestingly, epidermal fatty acid-binding **protein** (E-FABP) and fatty acid-binding **protein**, adipocyte-type (A-FABP), were detected in liver cells but not in hepatoma cells. The functional implication of the identified **proteins** was discussed.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 20 OF 42 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:228153 CAPLUS

DOCUMENT NUMBER: 132:332111

TITLE: Changes in **protein** synthesis and phosphorylation during microspore embryogenesis in Brassica napus

AUTHOR(S): Cordewener, Jan; Bergervoet, Jan; Liu, Chun-Ming
CORPORATE SOURCE: Plant Research International, Wageningen, 6700 AA, Neth.

SOURCE: Journal of Plant Physiology (2000), 156(2), 156-163
CODEN: JPPHEY; ISSN: 0176-1617

PUBLISHER: Urban & Fischer Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Changes in **protein** synthesis and phosphorylation during microspore embryogenesis in Brassica napus were investigated by two-dimensional (2-D) **gel** electrophoresis. The expression pattern of 6 **proteins** previously identified as putative markers for embryo initiation in microspore cultures was studied during later stages of embryo development. All of them were transiently expressed for the induction period (8 h to 2 days) and disappeared on the 5th day but two of them were expressed again at the later stage of embryogenesis (12th day). Major changes in the patterns of **protein** synthesis were observed 5 days after initiation of microspore embryogenesis. In this period of time embryogenic microspores have formed proembryos within their exine. Later stages of embryo development were not accompanied by major changes in 2-D **protein** patterns. Comparison of 2-D patterns of phosphorylated **proteins** revealed minor differences between embryogenic and non-embryogenic cultures, except for the level of phosphorylation of hsp70. A clear difference of extracellular secreted **proteins** was observed between embryogenic and non-embryogenic microspore cultures. This work provides a biochem. insight for the understanding of microspore embryogenesis at the **protein** level.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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Set	Items	Description

? s	heat()shock()protein?	
	132844	HEAT
	91472	SHOCK
	1712861	PROTEIN?
S1	21855	HEAT()SHOCK()PROTEIN?
? s	electrophoresis and s1	
	196277	ELECTROPHORESIS
	21855	S1
S2	1259	ELECTROPHORESIS AND S1
? s	(2())electrophoresis) and s1	
	3182451	2
	729009	D
	196277	ELECTROPHORESIS
	276	2(W)D(W)ELECTROPHORESIS
	21855	S1
S3	9	(2())ELECTROPHORESIS) AND S1
? t	s3/7/1-9	

3/7/1

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0015163322 BIOSIS NO.: 200500070387
Characterization of particulate proteins in Pacific surface waters
AUTHOR: Saijo Sachiko; Tanoue Eiichiro (Reprint)
AUTHOR ADDRESS: Grad Sch Environm StudiesDept Earth and Environm SciChikusa
Ku, Nagoya Univ, Furo Cho, Nagoya, Aichi, 4648601, Japan**Japan
AUTHOR E-MAIL ADDRESS: tanoue@ihas.nagoya-u.ac.jp
JOURNAL: Limnology and Oceanography 49 (4): p953-963 July 2004 2004
MEDIUM: print
ISSN: 0024-3590 (ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We investigated molecular characteristics of particulate proteins in Pacific surface waters using two-dimensional electrophoresis (2DE). Most proteinaceous materials estimated by dye-binding methods were characterized by the 2DE unresolved acidic materials with a broad range of molecular mass and the 2DE unresolved low molecular mass materials with a broad range of isoelectric point. The 2DE unresolved acidic and low molecular mass materials were considered to comprise peptides conjugated with acidic saccharides and degradation products (peptides) of proteins, respectively, which indicates that almost all proteins in living organisms failed to survive in detrital particulate organic matter (POM). Nevertheless, 23 discrete proteins were distinguished by the 2DE. Electrophoretic patterns of the discrete proteins indicated that they were a component of detrital POM. Three discrete proteins were subjected to N terminal amino acid sequence analysis. Two proteins out of three could not be determined because their N termini were blocked, and one protein was determined from the N terminus to the ninth amino acid residue. A homology search revealed that the N terminal amino acid

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sequence of the protein agreed completely with that of 70 kDa **heat shock protein** (HSP70) derived from photosynthetic organisms. HSP70 is a major member of the molecular chaperones that protect or repair proteins from damage under conditions of environmental stress. The occurrence of HSP70 in this study demonstrated that phytoplankton were able to induce the molecular chaperone(s). Clarification of factor(s) controlling induction of chaperones will enable us to assess the actual environmental stress on phytoplankton at the biomolecular level.

3/7/2

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0014657598 BIOSIS NO.: 200400028355

Characterization of spermatozoa surface antigens by antisperm antibodies and its influence on acrosomal exocytosis.

AUTHOR: Bohring Claudia (Reprint); Krause Walter

AUTHOR ADDRESS: Andrology, Deutschhausstrasse 9, D-35033, Marburg, Germany
**Germany

AUTHOR E-MAIL ADDRESS: bohring@mailier.uni-marburg.de

JOURNAL: American Journal of Reproductive Immunology 50 (5): p411-419

November 2003 2003

MEDIUM: print

ISSN: 1046-7408 (ISSN print)

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: PROBLEM: Antisperm antibodies (ASA) are the main cause of immunological infertility, they impair sperm functions by binding to the sperm membrane. The aim of this study was to characterize highly enriched sperm membrane proteins by **2D-electrophoresis** and to identify membrane antigens binding ASA and to evaluate the influence of ASA on the acrosome reaction (AR). METHOD OF STUDY: Sperm membrane proteins were separated by **2D-electrophoresis** and antigens were identified by immunoblotting with ASA from seminal plasma samples of infertile men. The influence of ASA on the AR were observed and determined by means of flowcytometry. RESULTS: A total of 18 antigens were identified by using ASA from seminal plasma. Six of the recognized proteins were analyzed by means of mass spectrometry and peptide matching: HSP70 and HSP70-2, disulfide-isomerase-ER60, caspase-3 and two subunits of the proteasome (component-C2 and zeta-chain). ASA from seminal plasma are able to enhance the AR in donor-spermatozoa. CONCLUSION: The biochemical identification of these proteins will be helpful to understand the mechanism by which ASA impair sperm function and the fertilization process. Spermatozoa, in which the AR was prematurely induced by ASA, will not be able to fertilize anymore.

3/7/3

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0014501924 BIOSIS NO.: 200300470643

The proteomics approach to find biomarkers in gastric cancer.

AUTHOR: Ryu Jin-Woo; Kim Hyung-jee (Reprint); Lee Young-Sun; Myong Na-Hye;

Hwang Cheol-Hoh; Lee Gae-Sung; Yom Heng-Cherl
AUTHOR ADDRESS: Department of Urology, College of Medicine, Dankook
University, San-29 Anseo-dong, Cheonan, 330-714, South Korea**South Korea
AUTHOR E-MAIL ADDRESS: killtumor@yahoo.co.kr
JOURNAL: Journal of Korean Medical Science 18 (4): p505-509 August 2003
2003
MEDIUM: print
ISSN: 1011-8934
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Gastric cancer is a very serious disease and is naturally resistant to many anticancer drugs. To reduce the mortality and improve the effectiveness of therapy, many studies have tried to find key biomarkers. Proteomic technologies are providing the tools needed to discover and identify disease-associating biomarkers. The proteomic study of gastric cancer establishes any specific events that lead to cancer, and it provides a direct way to define the true function of genes. Using two dimensional (2D) electrophoresis of the stomach cancer tissue, we have gained about 1,500 spots in each gel, and 140 protein spots also were identified. Among the identified proteins, there were seven over-expressed proteins in stomach cancer tissue: NSP3, transgelin, prohibitin, heat shock protein (hsp) 27 and variant, protein disulfide isomerase A3, unnamed protein product and glucose regulated protein. There were also seven under-expressed proteins in stomach cancer: Apolipoprotein A-1, p20, nucleoside diphosphate isomerase A, alpha 1 antitrypsin, desmin, serum albumin and serotransferrin.

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0014299988 BIOSIS NO.: 200300258632
Effect of cigarette smoking on endothelial cells: a proteomic approach.
AUTHOR: Raveendran M (Reprint); Wang J; Utama B; Dudley D; Wang X L
AUTHOR ADDRESS: Genetics, SW Fnd for Biomed Res, 7620 NW Loop 410, San Antonio, TX, 78227-5301, USA**USA
AUTHOR E-MAIL ADDRESS: mraveend@darwin.sfbr.org; jwang@darwin.sfbr.org; autama@darwin.sfbr.org; dudleyd@uthscsa.edu; xwang@darwin.sfbr.org
JOURNAL: FASEB Journal 17 (4-5): pAbstract No. 412.1 March 2003 2003
MEDIUM: e-file
CONFERENCE/MEETING: FASEB Meeting on Experimental Biology: Translating the Genome San Diego, CA, USA April 11-15, 2003; 20030411
SPONSOR: FASEB
ISSN: 0892-6638 (ISSN print)
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We observe that cigarette smoking causes endothelial dysfunction by inducing excess apoptosis, and the effect can be partially protected by prior eNOS activation. In this study, we systemically investigated protein changes in cigarette smoke extract (CSE) treated endothelial cells using a proteomic approach. HUVEC were treated with 0.01 cigarette

equivalents/ml CSE for 24hrs, with or without preconditioning by L-Arg (400(M, substrate for eNOS) or L-NAME (200(M, NOS inhibitor). Proteins were then harvested for %2%-D% electrophoresis% (O'Farrell method). The silver stained gels were scanned with a laser densitometer and subjected to computer analysis. The proteins with more than 4 fold changes were analyzed by MALDI-MS and matched with the profile of known proteins. To confirm the result the change in the protein level was also crosschecked by western blot. We were able to detect 325 proteins by silver staining after %2%-D% electrophoresis%. Among those, 33 proteins had more than 3 fold increases or decreases and 15 proteins had more than 4 fold changes when comparing the CSE treated with the control cells. HSP-70-Lamin B1, HSP-70, HSP 27, Alpha-actinin, Annexin 6, Annexin 2, Moesin, HSP gp96 and Laminin-binding protein were up regulated. Myosin light chain, Prolyl 4-hydroxylase, eIF4A, Alpha enolase, Alpha tubulin, and Alpha tubulin Glutaminase were down regulated.)The identified proteins represent several different pathways including the apoptosis and stress response to CSE exposure. This unbiased systemic approach provides more insights into the mechanisms mediating the biological effects by cigarette smoking.

3/7/5

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0014014727 BIOSIS NO.: 200200608238

Identification of iron-regulated outer membrane proteins of *Mannheimia haemolytica* by comparative %2%-D% electrophoresis%, Western blotting, and MALDI-TOF

AUTHOR: Zehr E S (Reprint); Tabatabai L B (Reprint); Frank G H (Reprint)

AUTHOR ADDRESS: Natl. Animal Disease Ctr., USDA, ARS, Ames, IA, USA**USA

JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 102 p286 2002 2002

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SPONSOR: American Society for Microbiology

ISSN: 1060-2011

DOCUMENT TYPE: Meeting; Meeting Abstract

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Background: *Mannheimia haemolytica* (MH) inhabits the tonsils and nasal passages of healthy cattle as a small portion of the normal bacterial flora. After transport or during viral-induced illnesses, MH serotype A1 can undergo a rapid, selective growth in the nasopharynx, and proceed to cause acute pneumonia. Vaccination with MH possessing expressed iron-regulated outer membrane proteins (IROMPs) has inhibited colonization of the nasopharynx. In vaccinated cattle, antibodies to IROMPs correlated with inhibition of MH colonization. A common mechanism for pathogens to obtain iron from the host is to up-regulate iron acquisition proteins. To study the role of IROMPs in colonization of the nasopharynx, IROMPs were isolated and identified. Methods: OMPs from MH grown in iron-restricted (brain heart infusion broth containing 2,2'-dipyridyl) and in iron-replete broth were treated with DNase and RNase, then precipitated with trichloroacetic acid. OMPs were subjected to %2%-D% electrophoresis% and compared using BioRad's

PD-Quest software. OMPs that were up-regulated in the iron-restricted medium (presumably IROMPs) were determined to be nonimmunoreactive or immunoreactive by Western blotting using convalescent bovine antiserum as a probe. Selected IROMPs were picked from gels, digested with trypsin, and analyzed by MALDI-TOF for identification using Prospector's MS-FIT software. Results: Thus far, two of the selected immunoreactive IROMPs have been identified as transferrin binding proteins, TbpA and TbpB. Additional up-regulated proteins are homologous to the TonB receptor, **heat shock proteins**, and transcription regulators of several bacterial species. Conclusion: We have combined **2D-D electrophoresis**, Western blotting, and mass spectroscopy to identify some nonimmunoreactive and immunoreactive IROMPs of MH. The proteins may be further utilized to study their role in MH colonization of the nasopharynx.

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0013740825 BIOSIS NO.: 200200334336

Recombinant autofluorescent landmarks for standardization of electrophoretic migration of proteins

AUTHOR: Einhauer Adelheid; Jungbauer Alois (Reprint)

AUTHOR ADDRESS: Institute of Applied Microbiology, University of Agricultural Sciences, Muthgasse 18, A-1190, Vienna, Austria**Austria

JOURNAL: Electrophoresis 23 (7-8): p1146-1152 April, 2002 2002

MEDIUM: print

ISSN: 0173-0835

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RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Unequivocal identification of unknown protein spot patterns in two-dimensional **2D-D electrophoresis** still represents a major problem when performing comparative studies of different **2D-D electrophoresis** gels. Inhomogeneity of gels due to variations in the gel casting procedure, electroendosmosis and heterogeneity of proteins are major contributions to variations in migration patterns. By fusing green fluorescent protein to a number of well-defined selected proteins (human lysozyme, initiation factor 5a (EIF5a), rapamycin-selective 25 kDa immunophilin (FKBP25), and **heat shock protein** 90 beta (hsp90)), the isoelectric points and the molecular mass were designed. Proteins were additionally tagged with the FLAG tag enabling rapid purification by immunoaffinity chromatography. The fusion proteins were expressed intracellularly in yeast to avoid heterogeneity caused by post-translational modifications. The quality and applicability was tested in 1-D and **2D-D electrophoresis**. Sharp bands or symmetric spots were obtained. The proteins are considered as a new generation of reference proteins for electrokinetic separation methods.

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0012034418 BIOSIS NO.: 199900294078

Identification of HSP-60 as the specific antigen of IgM produced by
BRG-lymphoma cells

AUTHOR: Musante Luca (Reprint); Ulivi Massimo; Cutrona Giovanna; Chiorazzi
Nicholas; Roncella Silvio; Candiano Giovanni; Ferrarini Manlio

AUTHOR ADDRESS: Dipartimento di Nefrologia, Istituto Giannina Gaslini,
Largo Gerolamo Gaslini, n. 5, 16247, Genova GE, Italy**Italy

JOURNAL: Electrophoresis 20 (4-5): p1092-1097 April-May, 1999 1999

MEDIUM: print

ISSN: 0173-0835

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: In previous studies we described a patient with Burkitt's lymphoma and AIDS, whose cells recognized a molecule expressed by normal and malignant breast cells. In the present study, we identified this antigen by two-dimensional (2D) electrophoresis and Western blotting using the antibody produced by lymphoma cells. The antigen so identified consisted of two clusters of spots with a molecular mass (Mr) of 60 and 50 kDa, respectively. Preparative immobilized pH gradient (IPG) was subsequently used to isolate the clusters of spots of higher molecular masses, from which peptide fragments of approximately 10 aa were separated on reverse-phase chromatography and sequenced. This procedure enabled the identification of the antigen recognized by the lymphoma cells as HSP-60. By means of serological analyses it was possible to identify the lower molecular mass cluster of spots as a molecule related to HSP-60. It is hypothesized that this molecule is a membrane form of HSP-60 that differs from HSP-60 in a COOH terminal portion.

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0009857525 BIOSIS NO.: 199598325358

Localization of heat shock protein on cell membranes of
Phaseolus vulgaris

AUTHOR: Liu Jian; Yang Xiao-He; Wu Xian-Rong

AUTHOR ADDRESS: Beijing Agric. Univ., Beijing 100094, China**China

JOURNAL: Acta Botanica Sinica 37 (2): p87-90 1995 1995

ISSN: 0577-7496

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: Chinese

ABSTRACT: Experiment was designed to investigate the expression of heat shock proteins (HSPs) in hypocotyls of Phaseolus vulgaris L. and HSPs localization on cell membranes by means of 35S-Met labelling, fluorography of SDS-PAGE and 2D electrophoresis. The results showed that 70 kD group HSPs were the major labelled proteins and the small HSPs accumulate largely in the fractions of plasma membrane and tonoplast membrane.

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0008708131 BIOSIS NO.: 199395010397

A possible role of %heat% %shock% %proteins% in human sperm motility

AUTHOR: Yang Rei-Chen (Reprint); Shen Meng-Ru; Chiang Po-Hui; Yang Shu-Ling
; Chen Shun-Sheng

AUTHOR ADDRESS: Dep. of Physiol., Kaohsiung Med. Coll., No. 100, Shih-Chuan
1st Rd., Kaohsiung City 807, Taiwan**Taiwan

JOURNAL: Kaohsiung Journal of Medical Sciences 8 (6): p299-305 1992

ISSN: 0257-5655

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The testicular spermatogenic stem and seminiferous tubular cells selectively synthesize %heat% %shock% %proteins% (Hsps) during heat stress. Hsps, synthesized from testicular cells and leukocytes, are identical in molecular masses as well as chemical properties. In this study, we induced the Hsps from leukocytes and investigated their in vitro effects on human sperm motility. Semen samples were divided into two parts, washed and unwashed. The whole blood was heated in 43 degree C for 15 minutes for induction of Hsps. A trans-membrane migration method was used to examine the effect of heated blood plasma on human sperm motility. The main heat-induced proteins of leukocytes were detected by %2%-D% %electrophoresis% and Coomassie blue stain. Leukocytes treated by heat produced a large amount of Hsp72 and Hsp80, while only a small amount was observed in that of nonheated leukocytes. The heated blood plasma inhibited motility of washed sperm in a manner that was dose-dependent. In the presence of seminal plasma fluid, however, the inhibitory effects of heated plasma on human sperm motility could not be observed. It was concluded that the heat-induced substance(s) from leukocytes, which being highly possible the Hsps, interfered the mobility of wash human sperm and the inhibition might be antagonized by seminal plasma.

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Set	Items	Description
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\$0.62	0.107	DialUnits File5
\$0.62		Estimated cost File5
\$0.62		Estimated cost this search
\$0.62		Estimated total session cost 0.107 DialUnits

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? b5		
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\$0.00	0.100	DialUnits File410
\$0.00		Estimated cost File410
\$0.02		TELNET
\$0.02		Estimated cost this search
\$0.64		Estimated total session cost 0.207 DialUnits

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91472		SHOCK
1712861		PROTEIN?
S1 21855		HEAT() SHOCK() PROTEIN?
? s 2()D()gel()electrophoresis		
3182451	2	
729009	D	
230674	GEL	
196277	ELECTROPHORESIS	
S2 443	2()D()GEL()ELECTROPHORESIS	
? s s1 and s2		
21855	S1	
443	S2	
S3 24	S1 AND S2	
? t s3/7/1-24		

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0015180932 BIOSIS NO.: 200500087997

Localization of the chaperone proteins GRP78 and HSP60 on the luminal surface of bovine oviduct epithelial cells and their association with spermatozoa

AUTHOR: Boilard M; Reyes-Moreno C; Lachance C; Massicotte L; Bailey J L; Sirard M-A; Leclerc P (Reprint)

AUTHOR ADDRESS: 10 Espinay, Quebec City, PQ, G1L 3L5, Canada**Canada

AUTHOR E-MAIL ADDRESS: Pierre.Leclerc@crsfa.ulaval.ca

JOURNAL: Biology of Reproduction 71 (6): p1879-1889 December 2004 2004

MEDIUM: print

ISSN: 0006-3363

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RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Upon their transit through the female genital tract, bovine spermatozoa bind to oviduct epithelial cells, where they are maintained alive for long periods of time until fertilization. Although carbohydrate components of the oviduct epithelial cell membrane are involved in these sperm/oviduct interactions, no protein candidate has been identified to play this role. To identify the oviduct factors involved in their survival, sperm cells were preincubated for 30 min with apical membranes isolated from oviduct epithelial cells, washed extensively, and further incubated for up to 12 h in the absence of apical membranes. During this incubation, sperm viability, motility, and acrosomal integrity were improved compared with cells preincubated in the absence of apical membranes. This suggests that, during the 30-min preincubation with apical membrane extracts, either an oviductal factor triggered intracellular events resulting in positive effects on spermatozoa or that such a factor strongly attached to sperm cells to promote a positive action. Similarly, spermatozoa were incubated with apical membranes isolated from oviduct epithelial cells labeled with (35S)-methionine and, upon extensive washes, proteins were separated by two-dimensional (2D) gel electrophoresis to identify the factors suspected to have beneficial effects on spermatozoa. The six major proteins, according to their signal intensity on the autoradiographic film, were extracted from a 2-D gel of oviduct epithelial cell proteins run in parallel and processed for N-terminal sequencing of the first 15 amino acids. Of these, one was identical to heat shock protein 60 (HSP60) and one to the glucose-regulated protein 78 (GRP78). Their identities and association with spermatozoa were confirmed using an antibody directed against these proteins. This paper reports the localization of both GRP78 and HSP60 on the luminal/apical surface of oviduct epithelial cells, their binding to spermatozoa, and the presence of endogenous HSP60 in the sperm midpiece.

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0015151458 BIOSIS NO.: 200500058523

Proteomic analyses of the response of Arabidopsis chloroplast proteins to high light stress

AUTHOR: Phee Bong-Kwan; Cho Jin-Hwan; Park Sebyul; Jung Jin Hee; Lee

Youn-Hyung; Jeon Jong-Seong; Bhoo Seong Hee (Reprint); Hahn Tae-Ryong

AUTHOR ADDRESS: Grad Sch Biotechnol, Kyung Hee Univ, Suwon, 449701, South Korea**South Korea

AUTHOR E-MAIL ADDRESS: shbhoo@khu.ac.kr; trhahn@khu.ac.kr
JOURNAL: Proteomics 4 (11): p3560-3568 November 2004 2004
MEDIUM: print
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RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Light is an essential environmental factor in the progression of plant growth and development but prolonged exposure to high levels of light stress can cause cellular damage and ultimately result in the death of the plant. Plants can respond defensively to this stress for a limited period and this involves changes to their gene expression profiles. Proteomic approaches were therefore applied to the study of the response to high light stress in the Arabidopsis thaliana plant species. Wild-type Arabidopsis was grown under normal light (100 $\mu\text{mol photons m}^{-2}\text{s}^{-1}$) conditions and then subjected to high light (1000 $\mu\text{mol photons m}^{-2}\text{s}^{-1}$) stress. Chloroplasts were then isolated from these plants and both soluble and insoluble proteins were extracted and subjected to two-dimensional (2D) gel electrophoresis. The resolved proteins were subsequently identified by matrix assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS) and comparative database analysis. 64 protein spots, which were identified as candidate factors that responded to high light stress, were then selected for analysis and 52 of these were successfully identified using MALDI-TOF-MS analysis. 35 of the 52 identified proteins were found to decrease their expression levels during high light stress and a further 14 of the candidate proteins had upregulated expression levels under these conditions. Most of the proteins that were downregulated during high light stress are involved in photosynthesis pathways. However, many of the 14 upregulated proteins were identified as previously well-known high light stress-related proteins, such as heat shock proteins (HSPs), dehydroascorbate reductase (DHAR), and superoxide dismutase (SOD). Three novel proteins that were more highly expressed during periods of high light stress but had no clear functional relationship to these conditions, were also identified in this study.

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0015131955 BIOSIS NO.: 200500039020

Glycolytic enzymes associated with the cell surface of Streptococcus pneumoniae are antigenic in humans and elicit protective immune responses in the mouse

AUTHOR: Ling E; Feldman G; Portnoi M; Dagan R; Overweg K; Mulholland F; Chalifa-Caspi V; Wells J; Mizrahi-Nebenzahl Y (Reprint)

AUTHOR ADDRESS: Med Ctr Dept Microbiol and Immunol Pediatr Infect Dis Unit, Soroka Univ, IL-84105, Beer Sheva, Israel**Israel

AUTHOR E-MAIL ADDRESS: ymizr@bgumail.bgu.ac.il

JOURNAL: Clinical and Experimental Immunology 138 (2): p290-298 November 2004 2004

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LANGUAGE: English

ABSTRACT: *Streptococcus pneumoniae* is a leading cause of otitis media, sinusitis, pneumonia, bacteraemia and meningitis worldwide. The drawbacks associated with the limited number of various capsular polysaccharides that can be included in the polysaccharide-based vaccines focuses much attention on pneumococcal proteins as vaccine candidates. We extracted an enriched cell wall fraction from *S. pneumoniae* WU2. Approximately 150 soluble proteins could be identified by 2D gel electrophoresis. The proteins were screened by 2D-Western blotting using sera that were obtained longitudinally from children attending day-care centres at 18, 30 and 42 months of age and sera from healthy adult volunteers. The proteins were further identified using matrix-assisted laser desorption/ionization-time of flight mass spectrometry. Seventeen proteins were antigenic in children and adults, of which 13 showed an increasing antibody response with age in all eight children analysed. Two immunogenic proteins, fructose-bisphosphate aldolase (FBA) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and a control protein with known low immunogenicity, *heat shock protein* 70 (DnaK), were expressed in *Escherichia coli*, purified and used to immunize mice. Mouse antibodies elicited to the recombinant (r) FBA and rGAPDH were cross-reactive with several genetically unrelated strains of different serotypes and conferred protection to respiratory challenge with virulent pneumococci. In addition, the FBA used in this study (NP_345117) does not have a human ortholog and warrants further investigation as a candidate for a pneumococcal vaccine. In conclusion, the immunoproteomics based approach utilized in the present study appears to be a suitable tool for identification of novel *S. pneumoniae* vaccine candidates

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0015107361 BIOSIS NO.: 200500014426

Genomic data for alternate production strategies. I. Identification of major contaminating species for cobalt+2 immobilized metal affinity chromatography

AUTHOR: Cai Ying; Moore Misty; Goforth Robyn; Henry Ralph; Beitle Robert (Reprint)

AUTHOR ADDRESS: Dept Chem Engrn, Univ Arkansas, 3202 Bell Engrn Ctr, Fayetteville, AR, 72701, USA**USA

JOURNAL: Biotechnology and Bioengineering 88 (1): p77-83 October 5, 2004 2004

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LANGUAGE: English

ABSTRACT: Recent advances in technology have allowed for the identification of complex protein mixtures in a rapid fashion. This report highlights the use of 2D gel electrophoresis, mass spectrometry, and database analysis to determine contaminating species of the *Escherichia coli* genome that are present during immobilized metal affinity chromatography (IMAC), highlighting Co+2 as the affinity ligand. Four proteins

(triosephosphate isomerase, alpha galactosidase, Hsp90, and glucosamine 6-phosphate synthase) constitute the majority of E. coli proteins that bind and potentially may coelute during chromatography. Results are discussed within the context of changes that when implemented could lead to an increase in IMAC efficiency, not by altering column conditions, but rather by changing the nature of the nuisance proteins that principally reduce column capacity and extend processing times. Such a study illustrates the use of proteome data to aid in bioprocess design.
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0015049513 BIOSIS NO.: 200400420302

Mechanisms of action of the antidepressants fluoxetine and the substance P antagonist L-000760735 are associated with altered neurofilaments and synaptic remodeling

AUTHOR: Guest Paul C (Reprint); Knowles Michael R; Molon-Noblot Sylvain; Salim Kamran; Smith David; Murray Fraser; Laroque Philippe; Hunt Stephen P; De Felipe Carmen; Rupniak Nadia M; McAllister George

AUTHOR ADDRESS: Neurosci Res Ctr, Merck Sharp and Dohme, Eastwick Rd, Harlow, Essex, CM20 2QR, UK**UK

JOURNAL: Brain Research 1002 (1-2): p1-10 March 26, 2004 2004

MEDIUM: print

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DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Antidepressants are widely prescribed in the treatment of depression, although the mechanism of how they exert their therapeutic effects is poorly understood. To shed further light on their mode of action, we have attempted to identify a common proteomic signature in guinea pig brains after chronic treatment with two different antidepressants. Both fluoxetine and the substance P receptor (NK1R) antagonist (SPA) L-000760735 altered cortical expression of multiple heat shock proteins along with neurofilaments and related proteins that are critical determinants of synaptic structure and function. Analysis of NK1R -/- mice showed similar alterations of neurofilaments confirming the specificity of the effects observed with chronic NK1R antagonist treatment. To determine if these changes were associated with structural modification of synapses, we carried out electron microscopic analysis of cerebral cortices from fluoxetine-treated guinea pigs. This showed an increase in the percentage of synapses with split postsynaptic densities (PSDs), a phenomenon that is characteristic of activity-dependent synaptic rearrangement. These findings suggest that cortical alterations of the neurofilament pathway and increased synaptic remodeling are associated with the mechanism of these two antidepressant drug treatments and may contribute to their psychotherapeutic actions. Copyright 2004 Elsevier BY All rights reserved.

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0015026427 BIOSIS NO.: 200400397216

Sinorhizobium meliloti metabolism in the root nodule: A proteomic perspective

AUTHOR: Djordjevic Michael A (Reprint)

AUTHOR ADDRESS: Res Sch Biol SciGenom Interact GrpARC Ctr Excellence
Integrat Legume Res, Australian Natl Univ, GPO Box 475, Canberra, ACT,
2601, Australia**Australia

AUTHOR E-MAIL ADDRESS: michael@rsbs.anu.edu.au

JOURNAL: Proteomics 4 (7): p1859-1872 July 2004 2004

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ISSN: 1615-9853 (ISSN print)

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RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The proteome of the model symbiotic bacterium, *Sinorhizobium meliloti* was examined to determine the enzymatic reactions and cell processes that occur when *S. meliloti* occupies the root nodules of *Medicago truncatula* and *Melilotus alba*. The proteomes of the nodule bacteria were compared to that of *S. meliloti* grown under laboratory cultured conditions as an additional control. All the detectable protein spots on the two-dimensional (2-D) gels between pH 4-7 were analyzed. In total, the identity of proteins in 1545 spots from 2-D gels was determined using peptide mass fingerprinting. There were clear differences in the proteome of nodule bacteria and cultured bacteria and putative nodule-specific and nodule suppressed proteins were identified. The data were analyzed using metabolic pathway prediction programs and used to review the biochemical and genetic studies that had been done previously on *S. meliloti* over several decades. There was a broad congruency between the proteomic and biochemical data when the overall pathways of central carbon and nitrogen metabolism were considered. A selective suite of ABC-type transporters was present in nodule bacteria that were biased towards the transport of amino acids and inorganic ions (P and Fe) suggesting that a highly specialized nutrient exchange was occurring between the nodule bacteria and the host. Proteins prominent in nodule bacteria were those involved in the pathways for vitamin synthesis and stress-related processes (chaperoning, heat shock, detoxification of reactive oxygen species, regulation of stress and osmo-regulation). Some of these proteins were found only in nodule bacteria. These results show the extent of the shift in metabolism that occurs when *S. meliloti* invades legume plants and establishes a nitrogen fixing symbiosis.

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0014897931 BIOSIS NO.: 200400268688

Nuclear matrix protein expressions in hepatocytes of normal and cirrhotic rat livers under normal and regenerating conditions

AUTHOR: Yun Jing-Ping (Reprint); Liew Choong-tsek; Chew Eng Ching; Yin Xiao-Yu; Lai Paul Bo San; Fai Yam Hin; Li H K Richard; Jin Mei-Lin; Ding Ming-Xiao; Li Ming-Tao; Lin Han-Liang; Lau Wan Yee

AUTHOR ADDRESS: Ctr CancDept Pathol, Natl Sun Yat Sen Univ, 651 E Dongfeng Rd, Guangzhou, 510060, China**China

AUTHOR E-MAIL ADDRESS: jpyun@gzsums.edu.cn

JOURNAL: Journal of Cellular Biochemistry 91 (6): p1269-1279 April 15, 2004 2004

MEDIUM: print

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LANGUAGE: English

ABSTRACT: We explored the feasibility of studying nuclear matrix protein (NMP) expressions of the hepatocytes in normal and cirrhotic rat livers with liver regeneration after partial hepatectomy. Sixteen Wistar healthy rats were studied with experimental liver regeneration and/or liver cirrhosis. Two-dimensional (2D) gel electrophoresis was used to generate these NMP compositions from these rat liver samples. Several antibodies against cytokeratin, vimentin, actin, B23, HNF4alpha, and heat shock protein 70 were used for identification by Western blot. Totally, 41 strongly stained protein spots were characterized on the 2-D gels. Thirty-four protein spots were detected in all of these rat livers, of which, cytokeratin, vimentin, actin, HNF4alpha, and heat shock protein 70 were identified. B23 was detected in the regenerated livers. Three protein spots (s33, s34, and s35) were detectable only in NMP preparation extracted from the regenerating rat livers after hepatectomy. Another three protein spots (s36, s37, and s38) were detectable only in NMP preparation extracted from thioacetamide-induced cirrhotic rat livers. Under these conditions including experimental liver regeneration and/or liver cirrhosis, Over thirty higher abundance NMPs of hepatocytes were consistently expressed and considered as common and basic NMPs. Some of the NMPs are specific for liver regeneration and may play a critical role in cell proliferation and cell cycle, and some are specific for liver cirrhosis. Copyright 2004 Wiley-Liss, Inc.

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0014776735 BIOSIS NO.: 200400157492

F-actin capping (CapZ) and other contractile saphenous vein smooth muscle proteins are altered by hemodynamic stress: A proteomic approach.

AUTHOR: McGregor Emma (Reprint); Kempster Lee; Wait Robin; Gosling Martin; Dunn Michael J; Powell Janet T

AUTHOR ADDRESS: South Wing Laboratory, Proteome Sciences plc, Institute of Psychiatry, 16 De Crespigny Park, London, SE5 8AF, UK**UK

AUTHOR E-MAIL ADDRESS: e.mcgregor@iop.kcl.ac.uk

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LANGUAGE: English

ABSTRACT: Increased force generation and smooth muscle remodeling follow the implantation of saphenous vein as an arterial bypass graft. Previously, we characterized and mapped 129 proteins in human saphenous

vein medial smooth muscle using two-dimensional (2-D) PAGE and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Here, we focus on actin filament remodeling in response to simulated arterial flow. Human saphenous vein was exposed to simulated venous or arterial flow for 90 min in vitro, and the contractile medial smooth muscle was dissected out and subjected to 2D-PAGE using a non-linear immobilized pH 3-10 gradient in the first dimension. Proteins were analyzed quantitatively using PDQuest 2-D software. The actin polymerization inhibitor cytochalasin B (1 μ M) prevented increases in force generation after 90 min of simulated arterial flow. At this time point, there were several consistent changes in actin filament-associated protein expression (seven paired vein samples). The heat shock protein HSP27, identified as a three-spot charge train, showed a 1.6-fold increase in abundance ($p=0.01$), but with reduced representation of the phosphorylated Ser82 and Ser15Ser82 isoforms ($p=0.018$). The abundance of actin-capping protein alpha2 subunit CapZ had decreased 3-fold, $p=0.04$. A 19-kDa proteolytic fragment of actin increased 2-fold, $p=0.04$. For the four-spot charge train of gelsolin, there was reduced representation of the more acidic isoforms, $p=0.022$. The abundance of other proteins associated with actin filaments, including cofilin and destrin, remained unchanged after arterial flow. Actin filament remodeling with differential expression and/or post-translational modification of proteins involved in capping the barbed end of actin filaments, HSP27 and CapZ, is an early response of contractile saphenous vein smooth muscle cells to hemodynamic stress. The observed changes would favor the generation of contractile stress fibers.

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0014763705 BIOSIS NO.: 200400131059

Phosphoproteome analysis of cardiomyocytes subjected to beta-adrenergic stimulation: Identification and characterization of a cardiac heat shock protein p20.

AUTHOR: Chu Guoxiang; Egnaczyk Gregory F; Zhao Wen; Jo Su-Hyun; Fan Guo-chang; Maggio John E; Xiao Rui-Ping; Kranias Evangelia G (Reprint)
AUTHOR ADDRESS: Department of Pharmacology and Cell Biophysics, College of Medicine, University of Cincinnati, 231 Albert B. Sabin Way, Cincinnati, OH, 45267-0575, USA**USA

AUTHOR E-MAIL ADDRESS: litsa.kranias@uc.edu

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ABSTRACT: Posttranslational modification of target substrates underlies biological processes through activation/inactivation of signaling cascades. To concurrently identify the phosphoprotein substrates associated with cardiac beta-adrenergic signaling, the mouse myocyte phosphoproteome was analyzed using 2D-PAGE using gel electrophoresis in combination with 32P autoradiography. Phosphoprotein spots, detected by silver staining, were identified using

MALDI-TOF mass spectrometry in conjunction with computer-assisted protein spot matching. Stimulation with isoproterenol (1 μ mol/L for 5 minutes) was associated with maximal increases in myocyte contractile parameters, and significant stimulation of the phosphorylation of troponin I (190+-23%) and succinyl CoA synthetase (160+-16%), whereas the phosphorylation of pyruvate dehydrogenase (48+-10%), NADH-ubiquinone oxidoreductase (46+-6%), **heat shock protein** 27 (18+-3%), alphaB-crystallin (20+-3%), and an unidentified 26-kDa protein (29+-7%) was significantly decreased, compared with unstimulated cells (100%). After sustained (30 minutes) stimulation with isoproterenol, only the alterations in the phosphorylation levels of troponin I and NADH-ubiquinone oxidoreductase were maintained and de novo phosphorylation of a phosphoprotein (approx 20 kDa and pI 5.5) was observed. The tryptic peptide fragments of this phosphoprotein were sequenced using postsource decay mass spectrometry, and the protein was subsequently cloned and designated as p20, based on its high sequence homology with rat and human skeletal p20. The mouse cardiac p20 contains the conserved domain sequences for **heat shock proteins**, and the RRAS consensus sequence for cAMP-PKA substrates. LC-MS/MS phosphorylation mapping confirmed phosphorylation of Ser16 in p20 on beta-agonist stimulation. Adenoviral gene transfer of p20 was associated with significant increases in contractility and Ca transient peak in adult rat cardiomyocytes, suggesting an important role of p20 in cardiac function. These findings suggest that cardiomyocytes undergo significant posttranslational modification via phosphorylation in a multitude of proteins to dynamically fine-tune cardiac responses to beta-adrenergic signaling.

3/7/10

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0014690671 BIOSIS NO.: 200400061428

Developmentally induced changes of the proteome in the protozoan parasite *Leishmania donovani*.

AUTHOR: Bente Meike; Harder Simone; Wiesgigl Martina; Heukeshoven Jochen; Gelhaus Christoph; Krause Eberhard; Clos Joachim; Bruchhaus Iris
(Reprint)

AUTHOR ADDRESS: Bernhard Nocht Institute for Tropical Medicine, Bernhard Nocht Str. 74, D-20359, Hamburg, Germany**Germany

AUTHOR E-MAIL ADDRESS: bruchhaus@bni.uni-hamburg.de

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ABSTRACT: In order to proceed through their life cycle, protozoan parasites of the genus *Leishmania* cycle between sandflies and mammals. This change of environment correlates with the differentiation from the promastigote stage (insect form) to the amastigote stage (intracellular mammalian form). The molecular basis underlying this major transformation is poorly understood so far; however, **heat shock protein** 90 (HSP90) appears to play a pivotal role. To further elucidate this process we identified proteins expressed preferentially in either of the two life

cycle stages. By using two-dimensional (2D) gel electrophoresis we observed defined changes in the protein pattern. A total of approximately 2000 protein spots were visualized. Of these, 31 proteins were present only in promastigotes. The abundance of 65 proteins increased during heat-induced in vitro amastigote differentiation, while a decreased abundance is observed for four proteins late in amastigote differentiation. Further analyses using matrix-assisted laser desorption/ionization-time of flight mass spectrometry and peptide mass fingerprinting 67 protein spots were identified representing 41 different proteins known from data-bases and eight hypothetical proteins. Further studies showed that most of the stage-specific proteins fall into five groups of functionally related proteins. These functional categories are: (i) stress response (e.g. heat, oxidative stress); (ii) cytoskeleton and cell membrane; (iii) energy metabolism and phosphorylation; (iv) cell cycle and proliferation; and (v) amino acid metabolism. Very similar changes in the 2-D protein pattern were obtained when in vitro amastigote differentiation was induced either by pharmacological inhibition of HSP90 or by a combination of heat stress and acidic pH supporting the critical role for HSP90 in life cycle control.

3/7/11

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0014595359 BIOSIS NO.: 200300551790

ANTI - 70 KD HEAT SHOCK PROTEIN AUTOANTIBODIES IN
PATIENTS WITH MULTIPLE EVANESCENT WHITE DOT SYNDROME

AUTHOR: Kachi S (Reprint); Nakamura M (Reprint); Nishizawa Y; Uemura A
(Reprint); Miyake Y (Reprint)

AUTHOR ADDRESS: Ophthalmology, Nagoya Univ School of Medicine, Nagoya-shi,
Japan**Japan

JOURNAL: ARVO Annual Meeting Abstract Search and Program Planner 2003 p
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20030504

SPONSOR: Association for Research in Vision and Ophthalmology

DOCUMENT TYPE: Meeting; Meeting Abstract

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Purpose To report the presence of autoantibodies against the 70 kD HEAT SHOCK PROTEIN in patients with multiple evanescent white dot syndrome (MEWDS). Methods Sera from two patients with MEWDS were subjected to Western blot analysis using bovine retinal proteins. The detected antigen was identified by two-dimensional (2D) gel electrophoresis, in-gel carboxymethylation and digestion, and mass spectrometry. Results A 70 kD bovine retinal antigen was recognized in the MEWDS sera by Western blot analysis. The protein was identified as a 70 kD HEAT SHOCK PROTEIN by mass spectrometry. The MEWDS sera recognized HEAT SHOCK PROTEIN 70 (Hsp70) and heat shock cognate protein 70 (Hsc70), which are expressed in the retina and are highly homologous with 95% of the amino acid residues identical. Conclusions The sera of the MEWDS patients contain autoantibodies against Hsp70 and Hsc70. This suggests that the

anti-70 kD %heat% %shock% %protein% autoantibody is a strong candidate for the cause of MEWDS. Mass spectrometry is a powerful tool to identify autoantigens in patients with possible autoimmune diseases.

3/7/12

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0014260934 BIOSIS NO.: 200300219653

Identification of cellular changes associated with increased production of human growth hormone in a recombinant Chinese hamster ovary cell line.

AUTHOR: Van Dyk Derek D (Reprint); Misztal David R; Wilkins Marc R;

Mackintosh James A; Poljak Anne; Varnai Jodie C; Teber Erdahl; Walsh

Bradley J; Gray Peter P

AUTHOR ADDRESS: Australian Proteome Analysis Facility, Macquarie University, 2109, Sydney, Australia**Australia

AUTHOR E-MAIL ADDRESS: dvandyk@proteome.org.au

JOURNAL: Proteomics 3 (2): p147-156 February 2003 2003

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LANGUAGE: English

ABSTRACT: A proteomics approach was used to identify the proteins potentially implicated in the cellular response concomitant with elevated production levels of human growth hormone in a recombinant Chinese hamster ovary (CHO) cell line following exposure to 0.5 mM butyrate and 80 µM zinc sulphate in the production media. This involved incorporation of two-dimensional (%2D-%D%) %gel% %electrophoresis% and protein identification by a combination of N-terminal sequencing, matrix-assisted laser desorption/ionisation-time of flight mass spectrometry, amino acid analysis and cross species database matching. From these identifications a CHO 2-D reference map and annotated database have been established. Metabolic labelling and subsequent autoradiography showed the induction of a number of cellular proteins in response to the media additives butyrate and zinc sulphate. These were identified as GRP75, enolase and thioredoxin. The chaperone proteins GRP78, HSP90, GRP94 and HSP70 were not up-regulated under these conditions.

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0014159644 BIOSIS NO.: 200300118363

Activation of platelet-derived growth factor pathway in human asthmatic pulmonary-derived mesenchymal cells.

AUTHOR: Malmstrom Johan; Tufvesson Ellen; Lofdahl Claes-Goran; Hansson

Lennart; Marko-Varga Gyorgy (Reprint); Westergren-Thorsson Gunilla

AUTHOR ADDRESS: Analytical Chemistry, Lund University, 221 00, Lund, Sweden
**Sweden

AUTHOR E-MAIL ADDRESS: gyorgy.marko-varga@astrazeneca.com

JOURNAL: Electrophoresis 24 (1): p276-285 January 2003 2003

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ABSTRACT: Cell cultures of mesenchymal type were obtained from biopsies taken after bronchoscopy from patients with asthma. It was possible to achieve outgrowth of fibroblast-like cells from these lung biopsies, which stained for alpha-smooth actin indicating that they were of myofibroblast type. Morphologically, two types of myofibroblasts could be observed: one intermediate form with more stretched cell shape and lamellipodia protrusions, and one more differentiated compact form of myofibroblast. The intermediate form was the most dominant type in these patients, indicating an active ongoing remodelling process. Further studies showed that platelet-derived growth factor (PDGF) might be the factor that stimulates the formation of the intermediate type of myofibroblasts, since it enhance migration of normal human lung fibroblasts 4-fold compared to control through an induced formation of stress fibers and lamellipodia protrusions. Additionally, intracellular signalling pathways involved in migration, such as RhoA and MAPkinase were stimulated 1.5-fold and 3.5-fold, respectively. By using two-dimensional (2D-D) gel electrophoresis and protein identification by peptide mass finger printing matrix assisted laser desorption/ionization - time of flight - mass-spectrometry (MALDI-TOF-MS) it was possible to confirm that PDGF affected the synthesis of proteins involved in the remodelling process, such as collagen VI and posttranslational forms thereof. PDGF also stimulated the production of FK506 binding protein of 65 kDa, a protein involved in smooth muscle differentiation, and proteins involved in the rearrangement of the cytoskeleton connected to migration such as the actin related protein ARP3, the T-complex protein and the heat shock protein 60. We demonstrate that PDGF has a potential pathological role in asthma and formation of subepithelial fibrosis by inducing changes in the proteome.

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0013689700 BIOSIS NO.: 200200283211
Protein expression during lag phase and growth initiation in *Saccharomyces cerevisiae*
AUTHOR: Brejning Jeanette (Reprint); Jespersen Lene
AUTHOR ADDRESS: Department of Dairy and Food Science, Food Microbiology,
The Royal Veterinary and Agricultural University, Rolighedsvej 30,
DK-1958, Frederiksberg C, Denmark**Denmark
JOURNAL: International Journal of Food Microbiology 75 (1-2): p27-38 5
May, 2002 2002
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ABSTRACT: In order to obtain a better understanding of the biochemical events taking place in *Saccharomyces cerevisiae* during the lag phase, the

proteins expressed during the first hours after inoculation were investigated by two-dimensional (2-D) gel electrophoresis and compared to those expressed in late respiratory growth phase. The studies were performed on a haploid strain (S288C) grown in defined minimal medium. Some of the abundant proteins, whose expression relative to total protein expression was induced during the lag phase, were identified by MALDI MS, and the expression of the corresponding genes was assessed by Northern blotting. The rate of protein synthesis was found to increase strongly during the lag phase and the number of spots detected on 2-D gels increased from 502 spots just after inoculation to 1533 spots at the end of the lag phase. During the first 20 min, the number of detectable spots was considerably reduced compared to the number of spots detected from the yeast in respiratory growth just prior to harvest and inoculation (747 spots), indicating an immediate pausing or shutdown in synthesis of many proteins just after inoculation. In this period, the cells got rid of most of their buds. The MALDI MS-identified, lag phase-induced proteins were adenosine kinase (Adolp), whose cellular role is presently uncertain, cytosolic acetaldehyde dehydrogenase (Ald6p) and (DL)-glycerol-3-phosphatase 1, both involved in carbohydrate metabolism, a ribosomal protein (Asc1p), a fragment of the 70-kDa heat shock protein Ssb1, and translationally controlled tumour protein homologue (Yk1056cp), all involved in translation, and S-adenosylmethionine synthetase 1 involved in biosynthesis reactions. The level of mRNA of the corresponding genes was found to increase strongly after inoculation. By pattern matching using previously published 2-D maps of yeast proteins, several other lag phase-induced proteins were identified. These were also proteins involved in carbohydrate metabolism, translation, and biosynthesis reactions. The identified proteins together with other, yet unidentified, lag phase-induced proteins are expected to be important for yeast growth initiation and could be valuable biological markers for yeast performance. Such markers would be highly beneficial in the control and optimisation of industrial fermentations.

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0013640006 BIOSIS NO.: 200200233517

Multiple-stress resistance in pressure resistant mutants of *Escherichia coli*

AUTHOR: Aertsen A (Reprint); Hauben K (Reprint); Michiels C (Reprint)

AUTHOR ADDRESS: Katholieke Universiteit Leuven, Heverlee, Belgium**Belgium

JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 101 p566 2001 2001

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ABSTRACT: High hydrostatic pressure has gained importance as a novel non-thermal preservation technique. However, we have recently reported

the isolation of spontaneous pressure resistant mutants (LMM1010, LMM1020, LMM1030) from a pressure-sensitive *E. coli* strain, MG1655 (Hauben et al., 1997, Appl. Environ. Microbiol. 63: 945-950). *E. coli* MG1655 and its pressure resistant mutants were analysed for their resistance to stresses commonly encountered in food environments. Although these mutants were isolated independently and solely on the basis of pressure resistance, they displayed a remarkable cross-resistance to heat, acid, oxidative and/or osmotic stress. The pattern of enhanced stress resistance differed for each mutant, but none of the mutants was found more sensitive than the parent strain under our challenge conditions. Analysis of the global pattern of protein synthesis by **2D-gel electrophoresis** revealed that mutants LMM1010 and LMM1030, but not LMM1020, produced increased levels of some **heat shock proteins**, including the chaperones GrpE and DnaK, during exponential growth and at the onset of stationary phase. On the other hand it was demonstrated that heat shock and osmotic shock were able to induce temporary pressure resistance in the wild-type strain. In conclusion we have reason to believe that the acquisition of pressure resistance is linked to improved survival upon exposure to other stress factors, and that pressure resistance could be mediated by the action of chaperones.

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0013557625 BIOSIS NO.: 200200151136

Small **heat shock protein** p26 associates with nuclear lamins and HSP70 in nuclei and nuclear matrix fractions from stressed cells

AUTHOR: Willsie Julia K; Clegg James S (Reprint)

AUTHOR ADDRESS: Section of Molecular and Cellular Biology, Bodega Marine Laboratory, University of California (Davis), Bodega Bay, CA, 94923, USA
**USA

JOURNAL: Journal of Cellular Biochemistry 84 (3): p601-614 2001 2001

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LANGUAGE: English

ABSTRACT: The small heat shock/ α -crystallin protein p26 undergoes nuclear translocation in response to stress in encysted embryos of the brine shrimp *Artemia franciscana*. About 50% of total p26 translocates to nuclei in embryos treated with heat shock or anoxia, and in embryo homogenates incubated at low pH. Nuclear fractionation shows that the majority of nuclear p26 and a nuclear lamin are associated with the nuclear matrix fraction. To further explore the roles of p26 and other HSPs in stabilizing nuclear matrix proteins (NMPs), nuclear matrices from control, and heat-shocked embryos were disassembled in urea and evaluated by one and two-dimensional **2D-gel electrophoresis** and Western immunoblotting after reassembling. Nuclear lamins were present only in reassembled fractions and, in the case of heat shock, p26 and HSP70 were also present. HSP90 was not detected in any nuclear fraction. Confocal microscopy on isolated nuclei and nuclear matrix preparations from control and heat-shocked embryos

showed that the majority of p26 and a nuclear lamin share similar nuclear distributions. The combination of microscopy and fractionation results suggests that p26 and HSP70 play a role in the protection of nuclear lamins within the nuclear matrix.

3/7/17

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0013118978 BIOSIS NO.: 200100290817

Defining the mycoplasma 'cytoskeleton': The protein composition of the Triton X-100 insoluble fraction of the bacterium *Mycoplasma pneumoniae* determined by 2D-gel electrophoresis and mass spectrometry

AUTHOR: Regula J T; Boguth G; Goerg A; Hegermann J; Mayer F; Frank R; Herrmann R (Reprint)

AUTHOR ADDRESS: Zentrum fuer molekulare Biologie Heidelberg (ZMBH)
Mikrobiologie, Universitaet Heidelberg, Im Neuenheimer Feld 282, D-69120, Heidelberg, Germany**Germany

JOURNAL: Microbiology (Reading) 147 (4): p1045-1057 April, 2001 2001

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ISSN: 1350-0872

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LANGUAGE: English

ABSTRACT: After treating *Mycoplasma pneumoniae* cells with the nonionic detergent Triton X-100, an undefined, structured protein complex remains that is called the 'Triton X-100 insoluble fraction' or 'Triton shell'. By analogy with eukaryotic cells and supported by ultrastructural analyses it is supposed that this fraction contains the components of a bacterial cytoskeleton-like structure. In this study, the composition of the Triton X-100 insoluble fraction was defined by electron microscopic screening for possible structural elements, and by two-dimensional (2D-gel electrophoresis) and MS to identify the proteins present. Silver staining of 2-D gels revealed about 100 protein spots. By staining with colloidal Coomassie blue, about 50 protein spots were visualized, of which 41 were identified by determining the mass and partial sequence of tryptic peptides of individual proteins. The identified proteins belonged to several functional categories, mainly energy metabolism, translation and heat-shock response. In addition, lipoproteins were found and most of the proteins involved in cytoadherence that were previously shown to be components of the Triton X-100 insoluble fraction. There were also 11 functionally unassigned proteins. Based on sequence-derived predictions, some of these might be potential candidates for structural components. Quantitatively, the most prevalent proteins were the heat-shock protein DnaK, elongation factor Tu and subunits alpha and beta of the pyruvate dehydrogenase complex (PdhA, PdhB), but definite conclusions regarding the composition of the observed structures can only be drawn after specific proteins are assigned to them, for example by immunocytochemistry.

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0012504939 BIOSIS NO.: 200000223252

Characterization of heat, oxidative, and acid stress responses in *Brucella melitensis*

AUTHOR: Teixeira-Gomes Ana P (Reprint); Cloeckaert Axel; Zygmunt Michel S

AUTHOR ADDRESS: Laboratoire de Pathologie Infectieuse et Immunologie,
Centre de Recherches de Tours, INRA, 37380, Nouzilly, France**France

JOURNAL: Infection and Immunity 68 (5): p2954-2961 May, 2000 2000

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ABSTRACT: *Brucella melitensis* is a facultative intracellular pathogen which is able to survive and replicate within phagocytic cells. Therefore, it has to adapt to a range of different hostile environments. In order to understand the mechanisms of intracellular survival employed by virulent *B. melitensis* 16M, an initial approach consisting of analysis of the differences in patterns of protein synthesis in response to heat, oxidative, and acid pH stresses by two-dimensional (2-D) polyacrylamide gel electrophoresis was used. Depending on the stress, this involved about 6.4 to 12% of the 676 protein spots detected in 2D-gel electrophoresis. On the basis of N-terminal sequence analysis and database searching, 19 proteins whose level of synthesis was up- or down-regulated by stress conditions were identified. Some of them were previously reported for *Brucella*, such as BvrR, DnaK, GroEL, and Cu-Zn superoxide dismutase (SOD). Eight other proteins closely matched proteins found in other bacteria: AapJ, alpha-ETF, ClpP, Fe and/or Mn SOD, malate dehydrogenase, IalB, 30S ribosomal protein S1, and pyruvate dehydrogenase E1 component beta subunit. Results indicated that *B. melitensis* could bring specific regulatory mechanisms into play in response to stress conditions. For example, the ribosome releasing factor in *B. melitensis* appeared to be a heat shock protein, whereas the ClpP protein, described as a heat shock protein for *Escherichia coli*, was strongly down-regulated in *B. melitensis* in response to heat stress. Some of the identified proteins and their potential specific regulation could be required for the adaptation of *B. melitensis* to environmental stresses encountered in phagocytic cells and possibly for bacterial virulence.

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0010883723 BIOSIS NO.: 199799517783

Hsp70 genes and heat shock factors during preimplantation phase of mouse development

AUTHOR: Christians E (Reprint); Michel E; Renard J-P

AUTHOR ADDRESS: Serv. d'Histol. d'Embryol., Fac. Med. Vet., Univ. Liege
ULg, 20 Blvd. de Colonster, B-4000 Liege, Belgium**Belgium

JOURNAL: CMLS Cellular and Molecular Life Sciences 53 (2): p168-178 1997
1997

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ABSTRACT: Heat shock genes are found in all organisms, and synthesis of **heat shock proteins** is induced by various stressors in nearly all the cells forming these organisms. However, a particular situation is noticed for hsp70 genes in mouse embryos at the beginning of their development. First, spontaneous expression of hsp70 is observed at the onset of zygotic genome activity. Second, inducible expression is delayed until morula or early blastocyst stages. A better understanding of both these points depends on a more careful analysis of hsp70 expression in relation to their major regulators, the heat shock factors. In this review, we will see how the development of the preimplantation embryo highlights the complexity of heat shock gene regulation involving trans-cis interactions and the cellular and nuclear environment.

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0009711980 BIOSIS NO.: 199598179813

The Heat-shock Response and Expression of **Heat-shock proteins** in Wheat under Diurnal Heat Stress and Field Conditions

AUTHOR: Nguyen Henry T (Reprint); Joshi Chandrashekhar P; Klueva Natalya; Weng Jian; Hendershot Kerry L; Blum Abraham

AUTHOR ADDRESS: Plant Mol. Genet. Lab., Dep. Plant Soil Sci. Inst.

Biotechnol., Texas Tech Univ., Lubbock, TX 79409, USA**USA

JOURNAL: Australian Journal of Plant Physiology 21 (6): p857-867 1994 1994

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LANGUAGE: English

ABSTRACT: The occurrence of **heat-shock proteins** (HSPs) in response to high temperature stress is a universal phenomenon in higher plants and has been well documented. However, in agriculturally important species, less is known about the expression of HSPs under natural environments. A review of the heat-shock response in wheat (*Triticum aestivum* L.) is presented and recent results on the expression of wheat HSPs under diurnal stress and field conditions are reported. In the field experiment, flag leaf blade temperatures were obtained and leaf blades collected for northern blot analysis using HSP 16.9 cDNA as a probe. Temperatures of leaf blades ranged from 32 to 35 degree C under the tested field conditions at New Deal near Lubbock, Texas. Messenger RNAs encoding a major class of low molecular weight HSPs, HSP 16.9, were detected in all wheat genotypes examined. The results suggested that HSPs are synthesized in response to heat stress under agricultural production, and furthermore, that HSPs are produced in wheats differing in geographic background. In the controlled growth chamber experiment. HSP expression in two wheat cultivars, Mustang (heat tolerant) and Sturdy (heat susceptible) were analysed to determine if wheat genotypes differing in heat tolerance differ in in vitro HSP synthesis (translatable HSP mRNAs) under a chronic, diurnal heat-stress regime. Leaf tissues were collected from seedlings over a time-course and poly (A)+ RNAs were isolated for in vitro translation and **2-D gel electrophoresis**. The protein profiles shown in the 2-D gel analysis revealed that there were not only quantitative differences of individual HSPs between these

two wheat lines, but also some unique HSPs which were only found in the heat tolerant line. This data provides evidence of a correlation between HSP synthesis and heat tolerance in wheat under a simulated field environment and suggests that further genetic analysis of HSPs in a segregating population is worthy of investigation. In conclusion, the results of this study provide an impetus for the investigation of the roles of HSP genes in heat tolerance in wheat.

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0009165554 BIOSIS NO.: 199497186839

Induction of a heat shock response (HSP 72) in rat embryos exposed to selected chemical teratogens

AUTHOR: Mirkes Philip E (Reprint); Doggett Barbar; Cornel Leanne

AUTHOR ADDRESS: Dep. Pediatr. RD-20, Univ. Washington, Seattle, WA 98195, USA**USA

JOURNAL: Teratology 49 (2): p135-142 1994 1994

ISSN: 0040-3709

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: A monoclonal antibody to the 72 kD %%%heat%%% %%%shock%%% %%%protein%%% (HSP 72), Western blot analysis and %%%2%%%-%%%D%%% %%%gel%%% %%%electrophoresis%%%/autoradiography were used to determine whether selected chemical teratogens induced the synthesis and accumulation of HSP 72 in postimplantation rat embryos exposed in vitro. The chemical teratogens studied include N-Acetoxy-2-acetylaminofluorene (N-Ac-AAF), cadmium chloride (CAD), cyclophosphamide (CP), sodium arsenite (AS), and sodium salicylate (SAL). Exposures to test chemicals were selected that produced obvious embryotoxicity characterized by abnormal development and growth retardation. Of the five chemical teratogens studied, AS and SAL induced the synthesis and accumulation of HSP 72 in day 10 rat embryos. The kinetics of HSP 72 accumulation, however, differed between AS- and SAL-treated embryos. Maximal levels of HSP 72 were observed 24 hours after AS exposure and 10 hours after SAL exposure. N-Ac-AAF, CD, and CP induced obvious embryotoxicity; however, none of these chemical teratogens induced HSP 72 at any of the timepoints assayed. Although only a small sample of chemical teratogens was studied, our results suggest that the heat shock response, characterized by the synthesis and accumulation of HSP 72, is not a general biomarker for chemical teratogens.

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0008195341 BIOSIS NO.: 199293038232

COMPARISON OF THE NUCLEAR AND CYTOSOLIC FORMS OF THE AH RECEPTOR FROM HEPA 1C1C7 CELLS CHARGE HETEROGENEITY AND ATP BINDING PROPERTIES

AUTHOR: PERDEW G H (Reprint)

AUTHOR ADDRESS: DEP FOODS NUTRITION, PURDUE UNIVERSITY, WEST LAFAYETTE, INDIANA 47907, USA**USA

JOURNAL: Archives of Biochemistry and Biophysics 291 (2): p284-290 1991
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RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: 2-[-1-2-5I]Iodo-7,8-dibromo-p-dioxin ([125I]Br2DpD) and 2-[125I]Iodo-3-azido-7,8-dibromo-p-dioxin ([125I]N3Br2-DpD) are both capable of binding to the Ah receptor (AhR) with a high degree of specificity in cultured Hepa 1c1c7 cells. After incubation with either [125I]N3Br2DpD or [125I]Br2DpD Hepa 1c1c7 cytosolic and high salt nuclear extracts were analyzed by sucrose density gradient analysis with the following results: (i) With both radioligands an .apprx. 9 S form of the AhR was observed in cytosolic extracts. (ii) Nuclear extracts labeled with [125I]N3Br2DpD revealed both .apprx. 6 S and .apprx. 9 S forms of the AhR. (iii). In contrast, analysis of nuclear extracts labeled with [125I]Br2DpD revealed only an .apprx. 6 S form of the AhR. The .apprx. 9 S [125I]N3Br2DpD-labeled AhR was preferentially extracted with 100 mM KCl from a nuclear fraction and mixed with monoclonal antibody 8D3, an anti-90-kDa ~~heat shock~~ ~~protein~~ antibody. Monoclonal antibody 8D3 was able to bind to the .apprx. 9 S nuclear form of the AhR and caused the receptor to sediment as a heavier complex on sucrose density gradients. This would indicate that the AhR can reside in the nucleus bound to 90-kDa ~~heat shock~~ ~~protein~~. The [125I]N3Br2DpD-labeled .apprx. 6 peak fractions were collected and subjected to denaturing two-dimensional gel electrophoresis. A comparison of [125I]N3Br2DpD-labeled cytosolic (9 S) AhR preparations with the nuclear (6 S) AhR by ~~2D~~ ~~gel~~ ~~electrophoresis~~ was performed. The cytosolic form of the AhR was present in an apparent pI range of 5.2-5.7; the nuclear form focused between 5.5 and 6.2. The [125I]N3Br2DpD-labeled nuclear extracts were incubated with ATP-agarose and 43% of the photoaffinity-labeled AhR bound to the affinity gel. In contrast, .apprx. threefold lower binding of [125I]N3Br2DpD-labeled receptor was obtained when GTP-, AMP-, or ADP-agarose was used. Only 2% of the [125I]N3Br2DpD-labeled cytosolic AhR was able to bind to ATP-agarose. These results suggest that after the AhR translocates into the nucleus the following biochemical changes occur: (i) The sedimentation value for the AhR changes from an .apprx. 9 S to an .apprx. 6 species. (ii) The AhR attains the ability to bind with specificity to ATP. (iii) The AhR undergoes a shift to a more basic pI.

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COMPREHENSIVE TWO-DIMENSIONAL GEL PROTEIN DATABASES OFFER A GLOBAL APPROACH TO THE ANALYSIS OF HUMAN CELLS THE TRANSFORMED AMNION CELLS AMA MASTER DATABASE AND ITS LINK TO GENOME DNA SEQUENCE DATA

AUTHOR: CELIS J E (Reprint); GESSER B; RASMUSSEN H H; MADSEN P; LEFFERS H; DEJGAARD K; HONORE B; OLSEN E; RATZ G; ET AL

AUTHOR ADDRESS: INST MED BIOCHEM AND BIOREGULATION RES CENTRE, OLE WORMS ALLE, BUILD 170, UNIVERSITY PARK, DK-8000 AARHUS C, DENMARK**DENMARK

JOURNAL: Electrophoresis 11 (12): p989-1071 1990

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ABSTRACT: A total of 3430 polypeptides (2592 cellular; 838 secreted) from transformed human amnion cells (AMA) labeled with [35S]methionine were separated and recorded using computer-aided two-dimensional (2D) gel electrophoresis. A master 2-D gel database of cellular protein information that includes both qualitative and quantitative annotations has been established. The protein numbers in this database differ from those reported in an earlier version (Celis et al. Leukemia 1988,2,561-602) as a result of changes in the scanning hardware. The reported information includes: percentage of total radioactivity recovered from the gels (based on quantitations of polypeptides labeled with a mixture of 16 14C-amino acids), protein name (including credit to investigators that aided identification, antibody against protein, cellular localization, (nuclear, 40S hnRNP, 20S snRNP U5, proteasomes, endoplasmic reticulum, mitochondria, Golgi, ribosomes, intermediate filaments, microfilaments and microtubules), levels in fetal human tissues, partial protein sequences (containing information on 48 human proteins microsequence so far), cell cycle-regulated proteins, proteins sensitive to interferons .alpha., .beta., and .gamma., heat shock proteins, annexins and phosphorylated proteins. The results presented should be considered as the initial phase of a joint effort between our laboratories to undertake a general and systematic analysis of human proteins. Using this integrated approach it will be possible to identify phenotype-specific proteins, to microsequence them and store the information in the database, to identify the corresponding genes, to search for homology with previously characterized proteins and to study the function of groups of proteins (pathways, organelles, etc.) that exhibit interesting regulatory properties. In particular, the 2-D gel protein database may become increasingly important in view of the concerted effort to map and sequence the entire human genome.

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HEAT-SHOCK PROTEIN SYNTHESIS AND ACCUMULATION IN DIPLOID WHEAT

AUTHOR: VIERLING R A (Reprint); NGUYEN H T

AUTHOR ADDRESS: DEP AGRONOMY, HORTICULTURE ENTOMOL, TEXAS TECH UNIV,
LUBBOCK, TEXAS 79409, USA**USA

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ABSTRACT: Plants synthesize a set of proteins, called heat-shock proteins (HSPs) under high-temperature stress. These proteins may play a role in the genetic control of thermal tolerance in plants. The objective of this study was to determine if genotype differences exist in the synthesis and accumulation of HSPs in diploid wheat *Triticum monococcum* L. Plants of three *T. monococcum* accessions

were heat shocked at 37.degree.C in a controlled condition for 1 h and HSPs were labeled in vivo with 35S-methionine for 3 h. Analysis of HSPs separated by two-dimensional (2D) gel electrophoresis showed qualitative and quantitative diversity of HSP synthesis in *T. monococcum*. In order to study HSP accumulation, plants were heat shocked at 37.degree.C for 8 h and 2-D separated HSPs were visualized by silver staining. Both qualitative and quantitative diversity of HSP accumulation was observed. Optical density (visible light) of 34 HSPs ranged from 0.33 to 44.64 on silver-stained gels and from 0.21 to 37.64 on labeled gels. Heat-shock proteins unique to individual accessions were identified. The identification of genetic variability in HSP synthesis within diploid wheat provides a useful tool for genetic and physiological studies of the role of HSPs in higher plants.

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S2	443	2() D() GEL() ELECTROPHORESIS
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0013557625 BIOSIS NO.: 200200151136

Small heat shock protein p26 associates with nuclear lamins and HSP70 in nuclei and nuclear matrix fractions from stressed cells

AUTHOR: Willsie Julia K; Clegg James S (Reprint)

AUTHOR ADDRESS: Section of Molecular and Cellular Biology, Bodega Marine Laboratory, University of California (Davis), Bodega Bay, CA, 94923, USA
**USA

JOURNAL: Journal of Cellular Biochemistry 84 (3): p601-614 2001 2001

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RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The small heat shock/alpha-crystallin protein p26 undergoes nuclear translocation in response to stress in encysted embryos of the brine shrimp *Artemia franciscana*. About 50% of total p26 translocates to nuclei in embryos treated with heat shock or anoxia, and in embryo homogenates incubated at low pH. Nuclear fractionation shows that the majority of nuclear p26 and a nuclear lamin are associated with the nuclear matrix fraction. To further explore the roles of p26 and other HSPs in stabilizing nuclear matrix proteins (NMPs), nuclear matrices from control, and heat-shocked embryos were disassembled in urea and evaluated by one and two-dimensional (2D) gel electrophoresis and Western immunoblotting after reassembling. Nuclear lamins were present only in reassembled fractions and, in the

case of heat shock, p26 and HSP70 were also present. HSP90 was not detected in any nuclear fraction. Confocal microscopy on isolated nuclei and nuclear matrix preparations from control and heat-shocked embryos showed that the majority of p26 and a nuclear lamin share similar nuclear distributions. The combination of microscopy and fractionation results suggests that p26 and HSP70 play a role in the protection of nuclear lamins within the nuclear matrix.

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